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OM protein - protein search, using sw model

Run on: October 16, 2005, 20:17:32 ; Search time 30 Seconds
(without alignments)
229.173 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGFSDEMTXLDXLAAXDPINWLXXTKITDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 846186 seqs, 185815562 residues

Total number of hits satisfying chosen parameters: 846186

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Pending Patents AA New:*

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSPFSDENMTXLDXIXXDFINWLXXRTIDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database.: Pandina-Database 33 Members

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSPFSDENWTYLDLAXXDFINWLXXRTDXX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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OM protein - protein search, using sw model

Run on: October 16, 2005, 20:17:32 ; Search time 30 Seconds
(without alignments)
229.173 Million cell updates/sec

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XXHADGSFSDENVTILDNLAXRDEINWLIQTITDXX 37

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 846186 seqs, 185815562 residues

Total number of hits satisfying chosen parameters: 846186

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:49:43 ; Search time 150.5 Seconds
(without alignments)
287.151 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPEDENNTIIDNLAXRDFINWLIQTITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:15:41 ; Search time 5962.5 Seconds
(without alignments)
253.325 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XXHADGSPSDENNTYLDYLAAXDFINMLXTKITDXX 37

Scoring table: BLOSUM62DX

| | |
|-------------|-------------|
| Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 |
| Fgapop 6.0 | Fgapext 7.0 |
| Delop 6.0 | Delext 7.0 |

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US10042746/runat.17102005.100128.4866/app.query.fasta.1
-DB=Pending_Patents_NA_Main -QFMT=fastap -SUFFIX=rpnm -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62DX -TRANS=human40.cdi
-LIST=200 -DOCCALIGN=200 -THR SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746@cgn.1.1.5523 @runat.17102005.100128.4866 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Database : Pending Patents NA Main:*

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 21:05:22 ; Search time 1126 Seconds
(without alignments)
459.127 Million cell updates/sec

Title: US-10-042-746-1
Perfect score: 155
Sequence: 1 XXHADGSPDEMTXLDLXAXDPFIMWLXXXTKTDXX 37

Scoring table: BIOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2682026 segs, 6986173828 residues

Total number of hits satisfying chosen parameters: 53640412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Command line parameters:

-MODEL=frame_p2n_model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10042746/runac_14102005_180155_4174/app_query_fasta.
-DB=pending_Patents_NA_New -QFMT=fastag -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blisum62DX -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=200
-MODE=LOCAL -OUTFMT=pco -NOM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746@cgn_1_1_247@runac_14102005_180155_4174 -NCPU=6 -ICPU=3
-NO MAP -LARGESQUDERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Pending_Patents_NA_New:*

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:17:30 ; Search time 490 Seconds
(without alignments)
529.404 Million cell updates/sec

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XXHADGFSDEMTIILDLAXRDPFNNWLIQTKITDXX 37

Scoring table: BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8766186 seqs, 3505510206 residues

Total number of hits satisfying chosen parameters: 17532372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DRV=r1h
-Q=/cgn2.1/USFTO_spool/US10042746/runat_17102005.100128.4884/app_query.fasta_1.3
-DB=published.Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=bl0sum62DX
-TRANS-human40.cgi -LIST=200 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=125 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000
-USER=US10042746.@CGC 1.1.582.@runat_17102005.100128.4884 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -MSG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 21:05:22 ; Search time 1126 Seconds.
(without alignments)
459.127 Million cell updates/sec

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XXHADGSFSDENATILDLNAXRDFINWLIQTKITDX 37

Scoring table: BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 26820206 segs, 6986173828 residues

Total number of hits satisfying chosen parameters: 53640412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US10042746/runat_14102005_180155_4174/app.query.fasta.1
-DB=Pending_Patents_NA_New -QFWT=fastap -SUFFIX=rnpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62DX -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=200
-MODE=LOCAL -OUTPMT=pro -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 @CGN 1 1 247 @runat_14102005_180155_4174 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY_NBS_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Tue Oct 18 16:18:23 2005

US-10-042-746-2.rupm

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:15:41 ; Search time 5962.5 seconds
(without alignments)

Title: US-10-042-746-2
Perfect score: 174
Sequence: 1 XCHADGFSFDEWNTIIDLNLAXRDFINWLIQTKITDX 37
253.325 Million cell updates/sec

Scoring table: BLOSUM62DX

| | |
|-------------|-------------|
| Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 |
| Fgapop 6.0 | Fgapext 7.0 |
| Delop 6.0 | Delext 7.0 |

Searched: 4554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US10042746/runat_17102005_100128_4866/app.query.fasta.1.3
-DB=Pending Patents NA.Main -QPMT=fastcap -SUFFIX=rupm -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62dx -TRANS=human40.cdi
-LIST=200 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125
-MODE=LOCAL -OUTPMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746.@CGN.1.1.5523@runat_17102005_100128_4866 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
-AFBASE .
Database: Pending Patents NA.Main.1

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 20:52:27 ; Search time 123.5 Seconds

(without alignments)
490.221 Million cell updates/sec

Title: US-10-042-746-2

Sequence: 1 XHAGSFSDEMTIINDNAXRDFIMWLQTKITDX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Command line parameters:

-MODE=frame+pn.model -DEV=xlh
-Q/cg2_1/USPTO.spool/US1004746/rnat 14102005 180154 4144/app query.fasta_1.398
-DB=Issued Patents NA -QFMT=fastap -SUFIX=rm1 -MINMATCH=0.1 -LOOPT=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=blomsu62dx -TRANS=human40.ccd
-LIST=200 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=200
-MODE=LOCAL -OUTFMT=ptc -NORTEXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1004746 -WCEN 1.1 93 -rnat 14102005 180154 4144 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cg2_6/prodata/1/ina/5A.COMB.seq: *
2: /cg2_6/prodata/1/ina/5B.COMB.seq: *
3: /cg2_6/prodata/1/ina/5A.COMB.seq: *
4: /cg2_6/prodata/1/ina/5B.COMB.seq: *
5: /cg2_6/prodata/1/ina/5A.COMB.seq: *
6: /cg2_6/prodata/1/ina/5B.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 174 | 100.0 | 895 | 3 | US-08-784-582-55 |
| 2 | 174 | 100.0 | 955 | 3 | US-08-784-582-55 |
| 3 | 174 | 100.0 | 955 | 3 | US-08-784-582-60 |
| 4 | 174 | 100.0 | 1062 | 4 | US-09-016-434-1212 |
| 5 | 174 | 100.0 | 2356 | 4 | US-08-784-582-72 |
| 6 | 76 | 43.7 | 207 | 1 | US-08-193-863-3 |
| 7 | 76 | 43.7 | 207 | 1 | US-08-377-833-3 |
| 8 | 76 | 43.7 | 207 | 1 | US-08-324-502-3 |
| 9 | 76 | 43.7 | 207 | 1 | US-08-083-501-3 |
| 10 | 76 | 43.7 | 207 | 1 | US-08-415-939-3 |
| 11 | 74 | 42.5 | 144 | 2 | US-08-835-231-17 |
| 12 | 74 | 42.5 | 144 | 3 | US-09-108-661-17 |

| | | | | | | |
|----|------|------|--------|---|----------------------|--------------------|
| 13 | 72 | 41.4 | 143 | 2 | US-08-835-231-14 | Sequence 14, Appl |
| 14 | 72 | 41.4 | 143 | 3 | US-09-108-661-14 | Sequence 14, Appl |
| 15 | 72 | 41.4 | 159 | 2 | US-08-835-231-15 | Sequence 15, Appl |
| 16 | 72 | 41.4 | 159 | 3 | US-09-108-661-15 | Sequence 15, Appl |
| 17 | 72 | 41.4 | 528 | 2 | US-08-835-231-7 | Sequence 7, Appl |
| 18 | 72 | 41.4 | 528 | 2 | US-08-835-231-8 | Sequence 8, Appl |
| 19 | 72 | 41.4 | 528 | 3 | US-09-108-661-7 | Sequence 7, Appl |
| 20 | 72 | 41.4 | 528 | 3 | US-09-108-661-8 | Sequence 8, Appl |
| 21 | 72 | 41.4 | 711 | 4 | US-09-949-016-3581 | Sequence 3581, Ap |
| 22 | 72 | 41.4 | 13795 | 4 | US-09-949-016-15323 | Sequence 15323, A |
| 23 | 72 | 40.8 | 110 | 1 | US-07-741-931-8 | Sequence 8, Appl |
| 24 | 71 | 40.8 | 110 | 1 | US-07-741-931-9 | Sequence 9, Appl |
| 25 | 71 | 40.8 | 110 | 1 | US-07-937-132A-8 | Sequence 8, Appl |
| 26 | 71 | 40.8 | 110 | 1 | US-07-937-132A-9 | Sequence 9, Appl |
| 27 | 71 | 40.8 | 255 | 4 | US-09-280-030-51 | Sequence 51, Appl |
| 28 | 70 | 40.2 | 561 | 2 | US-08-835-231-3 | Sequence 3, Appl |
| 29 | 70 | 40.2 | 561 | 2 | US-08-835-231-4 | Sequence 4, Appl |
| 30 | 70 | 40.2 | 561 | 3 | US-09-108-661-3 | Sequence 3, Appl |
| 31 | 70 | 40.2 | 561 | 3 | US-09-108-661-4 | Sequence 4, Appl |
| 32 | 69 | 39.7 | 87 | 1 | US-07-741-931-1 | Sequence 1, Appl |
| 33 | 69 | 39.7 | 87 | 1 | US-07-741-931-1 | Sequence 1, Appl |
| 34 | 69 | 39.7 | 87 | 4 | US-09-280-030-59 | Sequence 59, Appl |
| 35 | 66 | 37.9 | 107 | 1 | US-07-741-931-11 | Sequence 11, Appl |
| 36 | 66 | 37.9 | 107 | 1 | US-07-937-132A-11 | Sequence 11, Appl |
| 37 | 63 | 36.2 | 107 | 1 | US-07-741-931-10 | Sequence 10, Appl |
| 38 | 63 | 36.2 | 107 | 1 | US-07-937-132A-10 | Sequence 10, Appl |
| 39 | 59 | 33.9 | 492 | 4 | US-09-019-172-1 | Sequence 1, Appl |
| 40 | 58 | 33.3 | 138 | 4 | US-09-614-847-146 | Sequence 146, App |
| 41 | 58 | 33.3 | 1079 | 3 | US-08-789-328C-2 | Sequence 2, Appl |
| 42 | 58 | 33.3 | 1088 | 3 | US-08-789-328C-2 | Sequence 2, Appl |
| 43 | 58 | 33.3 | 6529 | 3 | US-08-789-328C-1 | Sequence 1, Appl |
| 44 | 57.5 | 33.0 | 1713 | 4 | US-09-489-039A-4371 | Sequence 4371, Ap |
| 45 | 57 | 32.8 | 891 | 4 | US-09-540-236-962 | Sequence 962, App |
| 46 | 57 | 32.8 | 1477 | 4 | US-09-949-016-1684 | Sequence 1684, Ap |
| 47 | 57 | 32.8 | 1511 | 4 | US-09-708-392-16 | Sequence 16, Appl |
| 48 | 57 | 32.8 | 1511 | 4 | US-09-708-392-18 | Sequence 18, Appl |
| 49 | 57 | 32.8 | 1511 | 4 | US-09-949-016-481 | Sequence 481, App |
| 50 | 57 | 32.8 | 2538 | 4 | US-09-543-681A-193 | Sequence 193, Appl |
| 51 | 57 | 32.8 | 269223 | 4 | US-09-596-002-41 | Sequence 41, Appl |
| 52 | 56 | 32.2 | 129 | 3 | US-08-789-328C-11 | Sequence 11, Appl |
| 53 | 56 | 32.2 | 138 | 3 | US-08-789-328C-12 | Sequence 12, Appl |
| 54 | 55 | 31.6 | 105 | 3 | US-08-995-369-6 | Sequence 6, Appl |
| 55 | 55 | 31.6 | 105 | 5 | PCT-US95-10075-6 | Sequence 6, Appl |
| 56 | 55 | 31.6 | 381 | 4 | US-09-513-999C-94568 | Sequence 34568, A |
| 57 | 55 | 31.6 | 1866 | 4 | US-08-489-039A-2085 | Sequence 2085, Ap |
| 58 | 55 | 31.6 | 580073 | 4 | US-08-545-528D-1 | Sequence 1, Appl |
| 59 | 54.5 | 31.3 | 1614 | 4 | US-09-252-991A-10453 | Sequence 10453, A |
| 60 | 54.5 | 31.3 | 3255 | 4 | US-09-252-991A-10617 | Sequence 10617, A |
| 61 | 54.5 | 31.3 | 3375 | 4 | US-09-252-991A-10239 | Sequence 10239, A |
| 62 | 54 | 31.0 | 765 | 4 | US-09-270-767-13413 | Sequence 13413, A |
| 63 | 54 | 31.0 | 1314 | 4 | US-09-543-681A-2105 | Sequence 2105, Ap |
| 64 | 54 | 31.0 | 3669 | 4 | US-09-774-558-235 | Sequence 235, App |
| 65 | 54 | 31.0 | 3784 | 1 | US-07-623-033-1 | Sequence 1, Appl |
| 66 | 54 | 31.0 | 4112 | 4 | US-09-799-451-706 | Sequence 706, App |
| 67 | 54 | 31.0 | 12860 | 4 | US-09-949-016-12223 | Sequence 12223, A |
| 68 | 54 | 31.0 | 12861 | 4 | US-09-949-016-13426 | Sequence 13426, A |
| 69 | 53.5 | 30.7 | 3779 | 3 | US-09-221-017B-247 | Sequence 247, App |
| 70 | 53 | 30.5 | 954 | 4 | US-09-540-236-1910 | Sequence 1910, Ap |
| 71 | 53 | 30.5 | 4358 | 4 | US-09-949-016-4533 | Sequence 4533, Ap |
| 72 | 53 | 30.5 | 4359 | 4 | US-09-949-016-725 | Sequence 725, App |
| 73 | 53 | 30.5 | 4359 | 4 | US-09-949-016-17507 | Sequence 17507, A |
| 74 | 53 | 30.5 | 31940 | 4 | US-09-556-002-13 | Sequence 13, Appl |
| 75 | 52.5 | 30.2 | 344 | 4 | US-09-270-767-1364 | Sequence 1364, Ap |
| 76 | 52.5 | 30.2 | 344 | 4 | US-09-270-767-16646 | Sequence 16646, Ap |
| 77 | 52 | 29.9 | 320 | 4 | US-09-513-999C-27903 | Sequence 27903, A |
| 78 | 52 | 29.9 | 366 | 3 | US-08-908-643C-54 | Sequence 54, Appl |
| 79 | 52 | 29.9 | 426 | 3 | US-08-908-643C-52 | Sequence 52, Appl |
| 80 | 52 | 29.9 | 498 | 3 | US-08-908-643C-50 | Sequence 50, Appl |
| 81 | 52 | 29.9 | 882 | 1 | US-08-628-291-3 | Sequence 3, Appl |
| 82 | 52 | 29.9 | 882 | 2 | US-09-128-722-3 | Sequence 3, Appl |
| 83 | 52 | 29.9 | 914 | 4 | US-09-270-767-9986 | Sequence 9986, Ap |
| 84 | 52 | 29.9 | 1204 | 1 | US-08-628-291-11 | Sequence 11, Appl |
| 85 | 52 | 29.9 | 1204 | 2 | US-09-128-722-11 | Sequence 11, Appl |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:10:34 ; Search time 373.5 Seconds
(without alignments)
586,427 Million cell updates/sec

Title: US-10-042-746-2
Sequence: 1 XHHADGSPDEKMTLIDNLAHXDPINWLTQKITDX 37

Scoring table:
BLOSUM62DX
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q/cgm2 1/USPTO.spool/US10042746/runcat.17102005.100127.4856/app_query.fasta.1.398
-DB=Geneseq.16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPTCL=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=-1 -MATRIX=blonsum62dx -TRANS=human40.cdi
-LIST=200 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 @CGN 1.1 586 @runcat.17102005.100127.4856 -NCPU=6 -ICPU=3
-NO MAMP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: N Geneseq.16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001s:*
6: geneseqn2002s:*
7: geneseqn2002bs:*
8: geneseqn2003s:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 174 | 100.0 | 449 | 6 | ABV98066 Human pan |
| 2 | 174 | 100.0 | 449 | 6 | ABV98700 Human pan |
| 3 | 174 | 100.0 | 517 | 6 | ABV98530 Human pan |
| 4 | 174 | 100.0 | 543 | 10 | ADFI6132 Human alb |
| 5 | 174 | 100.0 | 543 | 10 | ADFI5896 Human alb |

| | | | | | | |
|----|-----|-------|-----|----|----------|--------------------|
| 6 | 174 | 100.0 | 543 | 10 | ADFI5900 | ADFI5900 Human alb |
| 7 | 174 | 100.0 | 543 | 10 | ADFI6347 | ADFI6347 Human alb |
| 8 | 174 | 100.0 | 543 | 10 | ADFI6130 | ADFI6130 Human alb |
| 9 | 174 | 100.0 | 543 | 10 | ADFI6129 | ADFI6129 Human alb |
| 10 | 174 | 100.0 | 543 | 10 | ADFI6299 | ADFI6299 Human alb |
| 11 | 174 | 100.0 | 543 | 10 | ADFI5899 | ADFI5899 Human alb |
| 12 | 174 | 100.0 | 543 | 10 | ADFI6131 | ADFI6131 Human alb |
| 13 | 174 | 100.0 | 543 | 10 | ADFI6348 | ADFI6348 Human alb |
| 14 | 174 | 100.0 | 543 | 10 | ADFI6133 | ADFI6133 Human alb |
| 15 | 174 | 100.0 | 543 | 10 | ADFI5898 | ADFI5898 Human alb |
| 16 | 174 | 100.0 | 543 | 10 | ADFI6165 | ADFI6165 Human alb |
| 17 | 174 | 100.0 | 543 | 10 | ADFI6167 | ADFI6167 Human alb |
| 18 | 174 | 100.0 | 543 | 10 | ADFI6170 | ADFI6170 Human alb |
| 19 | 174 | 100.0 | 543 | 10 | ADFI6168 | ADFI6168 Human alb |
| 20 | 174 | 100.0 | 543 | 10 | ADFI6165 | ADFI6165 Human alb |
| 21 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 22 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 23 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 24 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 25 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 26 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 27 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 28 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 29 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 30 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 31 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 32 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 33 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 34 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 35 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 36 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 37 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 38 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 39 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 40 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 41 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 42 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 43 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 44 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 45 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 46 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 47 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 48 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 49 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 50 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 51 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 52 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 53 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 54 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 55 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 56 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 57 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 58 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 59 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 60 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 61 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 62 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 63 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 64 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 65 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 66 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 67 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 68 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 69 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 70 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 71 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 72 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 73 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 74 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 75 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 76 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 77 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |
| 78 | 174 | 100.0 | 543 | 10 | ADFI6172 | ADFI6172 Human alb |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:08:30 ; Search time 2836.5 Seconds

(without alignments)
632.062 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGFSDBNNTIIDLNXRPDINWLTQKITDX 37

Scoring table:
BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapext 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-Q/cgnt1/USPTO.spool/US10042746/runat 17102005 100127 4844/app.query.fasta_1.398
-DB=GenBml -QPMF=fastap -SUFFIX=ise -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62dx -TRANS=humand0 cdi -LIST=200
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125 -MODE=LOCAL
-OUTFM=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRS=US10042746 @CGN 1.1 3851 @runat 17102005 100127 4844 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPEXT=0
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml1:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------|----------------------|
| 1 | 174 | 100.0 | 243 10 | RATGIUS |
| 2 | 174 | 100.0 | 543 9 | BT006813 Rat glucago |
| 3 | 174 | 100.0 | 543 12 | BT007507 Rat glucago |
| 4 | 174 | 100.0 | 895 6 | AR108106 Sequence |

| | | | | |
|----|-----|-------|-----------|---------------------|
| 5 | 174 | 100.0 | 955 6 | AR108107 Sequence |
| 6 | 174 | 100.0 | 955 6 | AR108109 Sequence |
| 7 | 174 | 100.0 | 1034 6 | A31421 H. sapiens m |
| 8 | 174 | 100.0 | 1036 6 | CO729100 Sequence |
| 9 | 174 | 100.0 | 1053 10 | GPFG |
| 10 | 174 | 100.0 | 1062 6 | AR270649 Sequence |
| 11 | 174 | 100.0 | 1062 9 | HDMGLIC |
| 12 | 174 | 100.0 | 1134 9 | BC005278 |
| 13 | 174 | 100.0 | 2356 6 | AR108119 |
| 14 | 174 | 100.0 | 3798 6 | CO493428 |
| 15 | 174 | 100.0 | 4146 6 | CO414344 Sequence |
| 16 | 174 | 100.0 | 6455 9 | HSGLIC |
| 17 | 174 | 100.0 | 10050 9 | HSGLIC |
| 18 | 174 | 100.0 | 163681 9 | AC007750 |
| 19 | 174 | 100.0 | 223513 2 | AC111919 |
| 20 | 174 | 100.0 | 235433 2 | AC097841 |
| 21 | 173 | 99.4 | 145 6 | CO054796 Sequence |
| 22 | 173 | 99.4 | 145 6 | CO074044 Sequence |
| 23 | 173 | 99.4 | 145 6 | CO104933 Sequence |
| 24 | 173 | 99.4 | 145 6 | CO143637 Sequence |
| 25 | 173 | 99.4 | 145 6 | CO179117 Sequence |
| 26 | 173 | 99.4 | 145 6 | CO203473 Sequence |
| 27 | 173 | 99.4 | 145 6 | CO226837 Sequence |
| 28 | 173 | 99.4 | 145 6 | CO264982 Sequence |
| 29 | 173 | 99.4 | 145 6 | CO302070 Sequence |
| 30 | 173 | 99.4 | 145 6 | CO339262 Sequence |
| 31 | 169 | 97.1 | 241 10 | AY623893 |
| 32 | 169 | 97.1 | 668 10 | MMPROGLG |
| 33 | 169 | 97.1 | 1102 10 | BC012975 |
| 34 | 169 | 97.1 | 1116 10 | AF276754 |
| 35 | 169 | 97.1 | 1118 10 | HMG |
| 36 | 169 | 97.1 | 188169 10 | AL928576 |
| 37 | 169 | 97.1 | 209762 2 | AC115074 |
| 38 | 169 | 97.1 | 219014 4 | AC024141 |
| 39 | 166 | 95.4 | 574 4 | AY242124 |
| 40 | 166 | 95.4 | 1108 4 | BOVGS |
| 41 | 165 | 94.8 | 1104 10 | OCCGUT |
| 42 | 165 | 94.8 | 1133 4 | AF308439 |
| 43 | 161 | 92.5 | 1056 6 | AX147453 |
| 44 | 153 | 87.9 | 559 4 | AF529185 |
| 45 | 117 | 67.2 | 360 6 | CO049795 |
| 46 | 117 | 67.2 | 360 6 | CO064797 |
| 47 | 117 | 67.2 | 360 6 | CO091744 |
| 48 | 117 | 67.2 | 360 6 | CO130570 |
| 49 | 117 | 67.2 | 360 6 | CO169179 |
| 50 | 117 | 67.2 | 360 6 | CO198311 |
| 51 | 117 | 67.2 | 360 6 | CO213772 |
| 52 | 117 | 67.2 | 360 6 | CO252355 |
| 53 | 117 | 67.2 | 360 6 | CO289502 |
| 54 | 117 | 67.2 | 360 6 | CO326482 |
| 55 | 115 | 66.1 | 1186 5 | S78477 |
| 56 | 109 | 62.6 | 1360 5 | BC075391 |
| 57 | 105 | 60.3 | 984 5 | AY485816 |
| 58 | 104 | 59.8 | 922 5 | AY485817 |
| 59 | 104 | 59.8 | 922 5 | AY485820 |
| 60 | 104 | 59.8 | 1050 5 | HSU77612 |
| 61 | 103 | 59.2 | 1408 5 | AF004432 |
| 62 | 99 | 56.9 | 974 5 | AY485815 |
| 63 | 92 | 52.9 | 790 5 | AY485819 |
| 64 | 92 | 52.9 | 1300 5 | AF324209 |
| 65 | 92 | 52.9 | 738 5 | AF159708 |
| 66 | 90 | 51.7 | 796 5 | AF159707 |
| 67 | 89 | 51.1 | 1014 5 | OMU19914 |
| 68 | 89 | 51.1 | 1041 5 | OMU19917 |
| 69 | 89 | 51.1 | 1041 5 | S78475 |
| 70 | 88 | 50.6 | 520 5 | AY485818 |
| 71 | 87 | 50.6 | 1045 5 | AY485812 |
| 72 | 86 | 49.4 | 952 5 | AY485809 |
| 73 | 86 | 49.4 | 2491 5 | AY485821 |
| 74 | 86 | 46.6 | 65 6 | CO534905 |
| 75 | 80 | 46.0 | 383 5 | OMU19913 |
| 76 | 80 | 46.0 | 383 5 | OMU19920 |
| 77 | 80 | 46.0 | 400 5 | S78473 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-------------------|-------------------|---------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| AR108107 Sequence | AR108109 Sequence | A31421 H. sapiens m | CO729100 Sequence | D00014 Cavia porce | AR270649 Sequence | J04040 Human gluc | BC005278 Homo sapi | AR108119 Sequence | CO493428 Sequence | CO414344 Sequence | V01515 Human gene | X03991 Human gene | AC007750 Homo sapi | AC111919 Rattus no | AC097841 Rattus no | CO054796 Sequence | CO074044 Sequence | CO104933 Sequence | CO143637 Sequence | CO179117 Sequence | CO203473 Sequence | CO226837 Sequence | CO264982 Sequence | CO302070 Sequence | CO339262 Sequence | AY623893 Phodopus | Z46845 M. muscu | BC012975 Mus muscu | AF276754 Mus muscu | J00059 Syrian hams | AL928576 Mouse DNA | AC115074 Mus muscu | AC024141 Mus muscu | AY242124 Sus scro | K00107 Bovine panc | M57688 Octodon deg | AF308439 Canis fam | AX147453 Sequence | AF529185 Ovis arie | CO049795 Sequence | CO064797 Sequence | CO091744 Sequence | CO130570 Sequence | CO169179 Sequence | CO198311 Sequence | CO213772 Sequence | CO252355 Sequence | CO289502 Sequence | CO326482 Sequence | S78477 proglucagon | BC075391 Xenopus t | AY485816 Neocerato | AY485817 Signalus a | AY485820 Agkistrod | U77612 Heloderma s | AF004432 Xenopus l | AY485815 Protopier | AY485819 Bufo mari | AF324209 Hoplobatr | AF159708 Petromyzo | AF159707 Petromyzo | U19914 Oncorhynch | U19917 Oncorhynch | S78475 proglucagon | AY485818 Hydrorag | AY485812 Ictalurns | AY485809 Sebastes | AY485821 Sebastes | CO534905 Sequence | U19913 Oncorhynch | U19920 Oncorhynch | S78473 Oncorhynch |
|-------------------|-------------------|---------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 16:34:36 ; Search time: 2275 Seconds
(without alignments)
619.067 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPDEMTITLIDIAKDFINMLIQTITDX 37

Scoring table:
BLASTUP62DX
Xgapop 10.0, Xgapext 0.5
Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q=/cgm2_1/uspro.spool/US10042746/rnat.17102005.100049.4729/app.query.fasta.1.398
-DB=BSI -QMT=faetap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62dx -TRANS=human0.cdi -LIST=500
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=250 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10042746 @CGN 1.1 4385 @rnat.17102005.100049.4729 -NCPU=6 -ICPU=3
-NO MAP -LAB=RECURRY -NEG_SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 174 | 100.0 | 224 | 5 | BU951728 |
| 2 | 174 | 100.0 | 310 | 5 | BU074812 |
| 3 | 174 | 100.0 | 340 | 5 | BU075759 |
| 4 | 174 | 100.0 | 378 | 5 | BU949819 |
| 5 | 174 | 100.0 | 384 | 6 | CB178364 |
| 6 | 174 | 100.0 | 389 | 5 | BO632756 |
| 7 | 174 | 100.0 | 391 | 6 | CA777022 |
| 8 | 174 | 100.0 | 400 | 6 | CB068992 |
| 9 | 174 | 100.0 | 401 | 6 | CA949891 |

| | | | | | |
|----|-----|-------|-----|---|----------|
| 10 | 174 | 100.0 | 403 | 6 | CA946915 |
| 11 | 174 | 100.0 | 409 | 6 | CB070384 |
| 12 | 174 | 100.0 | 419 | 6 | BM836042 |
| 13 | 174 | 100.0 | 420 | 5 | BQ786903 |
| 14 | 174 | 100.0 | 421 | 7 | CB822370 |
| 15 | 174 | 100.0 | 425 | 6 | CB178016 |
| 16 | 174 | 100.0 | 428 | 5 | BQ271407 |
| 17 | 174 | 100.0 | 431 | 5 | BO632226 |
| 18 | 174 | 100.0 | 434 | 5 | BM352677 |
| 19 | 174 | 100.0 | 435 | 5 | BU074878 |
| 20 | 174 | 100.0 | 439 | 5 | BU077375 |
| 21 | 174 | 100.0 | 441 | 6 | CB842357 |
| 22 | 174 | 100.0 | 442 | 5 | BU786403 |
| 23 | 174 | 100.0 | 443 | 2 | AM190333 |
| 24 | 174 | 100.0 | 445 | 5 | CA865479 |
| 25 | 174 | 100.0 | 446 | 5 | BQ788028 |
| 26 | 174 | 100.0 | 450 | 6 | CA843073 |
| 27 | 174 | 100.0 | 450 | 6 | CA948774 |
| 28 | 174 | 100.0 | 451 | 4 | BM503895 |
| 29 | 174 | 100.0 | 452 | 6 | BQ765791 |
| 30 | 174 | 100.0 | 452 | 6 | CB067109 |
| 31 | 174 | 100.0 | 454 | 2 | AM243578 |
| 32 | 174 | 100.0 | 454 | 5 | BU078231 |
| 33 | 174 | 100.0 | 464 | 6 | CB178614 |
| 34 | 174 | 100.0 | 466 | 6 | CA848770 |
| 35 | 174 | 100.0 | 469 | 6 | CB069665 |
| 36 | 174 | 100.0 | 470 | 4 | BM505325 |
| 37 | 174 | 100.0 | 471 | 6 | CA948241 |
| 38 | 174 | 100.0 | 471 | 6 | BM312561 |
| 39 | 174 | 100.0 | 473 | 4 | BI439035 |
| 40 | 174 | 100.0 | 474 | 4 | BI467273 |
| 41 | 174 | 100.0 | 475 | 6 | CA777299 |
| 42 | 174 | 100.0 | 478 | 5 | BU785166 |
| 43 | 174 | 100.0 | 479 | 4 | BM312257 |
| 44 | 174 | 100.0 | 479 | 6 | CB825195 |
| 45 | 174 | 100.0 | 482 | 7 | CB067193 |
| 46 | 174 | 100.0 | 487 | 4 | BM312448 |
| 47 | 174 | 100.0 | 488 | 6 | BU786347 |
| 48 | 174 | 100.0 | 488 | 5 | CA841163 |
| 49 | 174 | 100.0 | 489 | 6 | BM509838 |
| 50 | 174 | 100.0 | 490 | 4 | BM504973 |
| 51 | 174 | 100.0 | 492 | 5 | BU952083 |
| 52 | 174 | 100.0 | 492 | 6 | CA777272 |
| 53 | 174 | 100.0 | 494 | 4 | BI791789 |
| 54 | 174 | 100.0 | 495 | 5 | BQ271348 |
| 55 | 174 | 100.0 | 496 | 4 | BI712848 |
| 56 | 174 | 100.0 | 497 | 4 | BI438781 |
| 57 | 174 | 100.0 | 498 | 6 | CB068518 |
| 58 | 174 | 100.0 | 499 | 6 | CA948911 |
| 59 | 174 | 100.0 | 499 | 6 | CA950017 |
| 60 | 174 | 100.0 | 501 | 4 | BI712915 |
| 61 | 174 | 100.0 | 501 | 6 | CA941615 |
| 62 | 174 | 100.0 | 504 | 4 | BM504973 |
| 63 | 174 | 100.0 | 506 | 4 | EG655424 |
| 64 | 174 | 100.0 | 507 | 5 | BU949129 |
| 65 | 174 | 100.0 | 508 | 4 | BG655984 |
| 66 | 174 | 100.0 | 508 | 5 | BU072728 |
| 67 | 174 | 100.0 | 508 | 6 | CA776542 |
| 68 | 174 | 100.0 | 509 | 4 | BI715328 |
| 69 | 174 | 100.0 | 509 | 4 | BM315096 |
| 70 | 174 | 100.0 | 511 | 5 | BQ632620 |
| 71 | 174 | 100.0 | 512 | 6 | CA848560 |
| 72 | 174 | 100.0 | 513 | 5 | BU950509 |
| 73 | 174 | 100.0 | 515 | 6 | CA867509 |
| 74 | 174 | 100.0 | 515 | 6 | CA952216 |
| 75 | 174 | 100.0 | 516 | 6 | CA777150 |
| 76 | 174 | 100.0 | 516 | 6 | CB067101 |
| 77 | 174 | 100.0 | 519 | 4 | BM311172 |
| 78 | 174 | 100.0 | 521 | 4 | BG655407 |
| 79 | 174 | 100.0 | 522 | 6 | CA842549 |
| 80 | 174 | 100.0 | 522 | 6 | CA943101 |
| 81 | 174 | 100.0 | 523 | 4 | BM310964 |
| 82 | 174 | 100.0 | 525 | 6 | CA841460 |

| | |
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| CA946915 | 1612f03.x |
| CB070384 | 1636e05.y |
| BM836042 | K-EST0111 |
| BQ786903 | 1151c09.x |
| CB822370 | 1986a01.x |
| CB178016 | 1624a06.x |
| BQ271407 | 1K13e06.y |
| BO632226 | 1124b11.x |
| BM352677 | 1959g02.x |
| BU074878 | 1m77h03.y |
| BU077375 | 1m20e01.y |
| CB842357 | 1r26a06.y |
| BU786403 | 1m54e01.y |
| AM190333 | 1140g07.x |
| CA865479 | 1140g07.x |
| BQ788028 | 1146g09.x |
| CA843073 | 1r53g03.y |
| CA948774 | 1q27f01.y |
| BM503895 | 1997d05.y |
| BQ765791 | 1134g04.x |
| CB067109 | 1q32b10.y |
| AM243578 | 1033a10.x |
| BU078231 | 1m66a12.y |
| CB178614 | 1r37f01.x |
| CA848770 | 1r25c05.y |
| CB069665 | 1826f05.x |
| BI791800 | 1604g03.y |
| BM505325 | 1993d01.x |
| CA948241 | 1q19g03.y |
| BM312561 | 1g76d07.y |
| BI439035 | 1c25g02.y |
| BI467273 | 1c22c02.x |
| CA777299 | 1p05h04.y |
| BU785166 | 1n41h01.y |
| BM312257 | 1941b09.y |
| CB067193 | 1q33d04.y |
| CB825195 | 1946g01.y |
| BM312448 | 1c78f12.x |
| BU786347 | 1m53g03.y |
| CA841163 | 1p30d08.y |
| BM509838 | 1944f02.y |
| BU952083 | 1n73d05.y |
| CA777272 | 1o84b04.y |
| BI791789 | 1e04e11.y |
| BQ271348 | 1K12f12.y |
| BI712848 | 1d98a01.y |
| BI438781 | 1c26f01.x |
| CB069518 | 1816c04.y |
| CA948911 | 1q29g09.y |
| CA950017 | 1r65f08.y |
| BI712915 | 1d98h02.y |
| CA941615 | 1r31f10.y |
| BM504973 | 1988g06.y |
| BG655424 | 1b34c02.y |
| BU949129 | 1m66c06.x |
| BG655984 | 1b56c10.y |
| BU072728 | 1m46h11.y |
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| BI715328 | 1c31f04.y |
| BM315096 | 1943d08.y |
| BQ632620 | 1125f03.y |
| CA848560 | 1p36d02.y |
| BU950509 | 1o78c02.y |
| CA867509 | 1r12g03.y |
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| CA777150 | 1p03g09.y |
| CB067101 | 1q32a11.y |
| BM311172 | 1p61g03.y |
| BG655407 | 1b39h07.y |
| CA842549 | 1q33g10.y |
| CA943101 | 1p38e09.y |
| BM310964 | 1958a05.y |
| CA841460 | 1q44b03.x |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2005, 15:17:48 ; Search time 54.5 Seconds

(without alignments)
282.986 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XH7ADGSPDEMTILNAXRPFIMWLTQITDX 37Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Published Applications AA:*
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep:*
11: /cgn2_6/prodata/2/pubpaa/US09C_NEW_PUB.pep:*
12: /cgn2_6/prodata/2/pubpaa/US09C_NEW_PUB.pep:*
13: /cgn2_6/prodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/prodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/2/pubpaa/US10E_NEW_PUB.pep:*
19: /cgn2_6/prodata/2/pubpaa/US11_PUBCOMB.pep:*
20: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 174 | 100.0 | 37 | 14 | US-10-042-746-2 |
| 2 | 174 | 100.0 | 37 | 15 | US-10-393-524A-11 |
| 3 | 174 | 100.0 | 180 | 16 | US-10-793-677-1 |
| 4 | 174 | 100.0 | 180 | 17 | US-10-775-180-198 |
| 5 | 174 | 100.0 | 180 | 17 | US-10-775-180-199 |
| 6 | 174 | 100.0 | 180 | 17 | US-10-775-180-200 |
| 7 | 174 | 100.0 | 180 | 17 | US-10-775-180-201 |
| 8 | 174 | 100.0 | 180 | 17 | US-10-775-180-202 |
| 9 | 174 | 100.0 | 180 | 17 | US-10-775-180-426 |
| 10 | 174 | 100.0 | 180 | 17 | US-10-775-180-427 |
| 11 | 174 | 100.0 | 180 | 17 | US-10-775-180-428 |

| | | | | | | |
|----|-----|-------|-----|----|--------------------|--------------------|
| 12 | 174 | 100.0 | 180 | 17 | US-10-775-180-430 | Sequence 430, App |
| 13 | 174 | 100.0 | 180 | 17 | US-10-775-180-651 | Sequence 651, App |
| 14 | 174 | 100.0 | 180 | 17 | US-10-775-180-675 | Sequence 675, App |
| 15 | 174 | 100.0 | 180 | 17 | US-10-775-180-676 | Sequence 676, App |
| 16 | 174 | 100.0 | 180 | 17 | US-10-871-709-2 | Sequence 2, App1 |
| 17 | 174 | 100.0 | 180 | 18 | US-10-775-204-630 | Sequence 630, App |
| 18 | 174 | 100.0 | 180 | 18 | US-10-775-204-632 | Sequence 632, App |
| 19 | 174 | 100.0 | 180 | 18 | US-10-775-204-633 | Sequence 633, App |
| 20 | 174 | 100.0 | 180 | 18 | US-10-775-204-634 | Sequence 634, App |
| 21 | 174 | 100.0 | 180 | 18 | US-10-775-204-1246 | Sequence 1246, App |
| 22 | 174 | 100.0 | 180 | 18 | US-10-775-204-1247 | Sequence 1247, App |
| 23 | 174 | 100.0 | 180 | 18 | US-10-775-204-1248 | Sequence 1248, App |
| 24 | 174 | 100.0 | 180 | 18 | US-10-775-204-1249 | Sequence 1249, App |
| 25 | 174 | 100.0 | 180 | 18 | US-10-775-204-1250 | Sequence 1250, App |
| 26 | 174 | 100.0 | 180 | 18 | US-10-775-204-1251 | Sequence 1251, App |
| 27 | 174 | 100.0 | 180 | 18 | US-10-775-204-1252 | Sequence 1252, App |
| 28 | 174 | 100.0 | 180 | 18 | US-10-775-204-1253 | Sequence 1253, App |
| 29 | 174 | 100.0 | 180 | 18 | US-10-775-204-1254 | Sequence 1254, App |
| 30 | 174 | 100.0 | 180 | 18 | US-10-775-204-1255 | Sequence 1255, App |
| 31 | 174 | 100.0 | 180 | 18 | US-10-775-204-1256 | Sequence 1256, App |
| 32 | 174 | 100.0 | 180 | 18 | US-10-775-204-1257 | Sequence 1257, App |
| 33 | 174 | 100.0 | 180 | 18 | US-10-775-204-1258 | Sequence 1258, App |
| 34 | 174 | 100.0 | 180 | 18 | US-10-775-204-1259 | Sequence 1259, App |
| 35 | 174 | 100.0 | 180 | 18 | US-10-775-204-1260 | Sequence 1260, App |
| 36 | 174 | 100.0 | 180 | 18 | US-10-775-204-1261 | Sequence 1261, App |
| 37 | 174 | 100.0 | 180 | 18 | US-10-775-204-1262 | Sequence 1262, App |
| 38 | 174 | 100.0 | 180 | 18 | US-10-775-204-1263 | Sequence 1263, App |
| 39 | 174 | 100.0 | 180 | 18 | US-10-775-204-1264 | Sequence 1264, App |
| 40 | 174 | 100.0 | 180 | 18 | US-10-775-204-1265 | Sequence 1265, App |
| 41 | 174 | 100.0 | 180 | 18 | US-10-775-204-1266 | Sequence 1266, App |
| 42 | 174 | 100.0 | 180 | 18 | US-10-775-204-1267 | Sequence 1267, App |
| 43 | 174 | 100.0 | 180 | 18 | US-10-775-204-1268 | Sequence 1268, App |
| 44 | 174 | 100.0 | 180 | 18 | US-10-775-204-1269 | Sequence 1269, App |
| 45 | 174 | 100.0 | 180 | 18 | US-10-775-204-1270 | Sequence 1270, App |
| 46 | 174 | 100.0 | 180 | 18 | US-10-775-204-1271 | Sequence 1271, App |
| 47 | 174 | 100.0 | 180 | 18 | US-10-775-204-1272 | Sequence 1272, App |
| 48 | 174 | 100.0 | 180 | 18 | US-10-775-204-1273 | Sequence 1273, App |
| 49 | 174 | 100.0 | 180 | 18 | US-10-775-204-1274 | Sequence 1274, App |
| 50 | 174 | 100.0 | 180 | 18 | US-10-775-204-1275 | Sequence 1275, App |
| 51 | 174 | 100.0 | 180 | 18 | US-10-775-204-1276 | Sequence 1276, App |
| 52 | 174 | 100.0 | 180 | 18 | US-10-775-204-1277 | Sequence 1277, App |
| 53 | 174 | 100.0 | 180 | 18 | US-10-775-204-1278 | Sequence 1278, App |
| 54 | 174 | 100.0 | 180 | 18 | US-10-775-204-1279 | Sequence 1279, App |
| 55 | 174 | 100.0 | 180 | 18 | US-10-775-204-1280 | Sequence 1280, App |
| 56 | 174 | 100.0 | 180 | 18 | US-10-775-204-1281 | Sequence 1281, App |
| 57 | 174 | 100.0 | 180 | 18 | US-10-775-204-1282 | Sequence 1282, App |
| 58 | 174 | 100.0 | 180 | 18 | US-10-775-204-1283 | Sequence 1283, App |
| 59 | 174 | 100.0 | 180 | 18 | US-10-775-204-1284 | Sequence 1284, App |
| 60 | 174 | 100.0 | 180 | 18 | US-10-775-204-1285 | Sequence 1285, App |
| 61 | 174 | 100.0 | 180 | 18 | US-10-775-204-1286 | Sequence 1286, App |
| 62 | 174 | 100.0 | 180 | 18 | US-10-775-204-1287 | Sequence 1287, App |
| 63 | 174 | 100.0 | 180 | 18 | US-10-775-204-1288 | Sequence 1288, App |
| 64 | 174 | 100.0 | 180 | 18 | US-10-775-204-1289 | Sequence 1289, App |
| 65 | 174 | 100.0 | 180 | 18 | US-10-775-204-1290 | Sequence 1290, App |
| 66 | 174 | 100.0 | 180 | 18 | US-10-775-204-1291 | Sequence 1291, App |
| 67 | 174 | 100.0 | 180 | 18 | US-10-775-204-1292 | Sequence 1292, App |
| 68 | 174 | 100.0 | 180 | 18 | US-10-775-204-1293 | Sequence 1293, App |
| 69 | 174 | 100.0 | 180 | 18 | US-10-775-204-1294 | Sequence 1294, App |
| 70 | 174 | 100.0 | 180 | 18 | US-10-775-204-1295 | Sequence 1295, App |
| 71 | 174 | 100.0 | 180 | 18 | US-10-775-204-1296 | Sequence 1296, App |
| 72 | 174 | 100.0 | 180 | 18 | US-10-775-204-1297 | Sequence 1297, App |
| 73 | 174 | 100.0 | 180 | 18 | US-10-775-204-1298 | Sequence 1298, App |
| 74 | 174 | 100.0 | 180 | 18 | US-10-775-204-1299 | Sequence 1299, App |
| 75 | 174 | 100.0 | 180 | 18 | US-10-775-204-1300 | Sequence 1300, App |
| 76 | 174 | 100.0 | 180 | 18 | US-10-775-204-1301 | Sequence 1301, App |
| 77 | 174 | 100.0 | 180 | 18 | US-10-775-204-1302 | Sequence 1302, App |
| 78 | 174 | 100.0 | 180 | 18 | US-10-775-204-1303 | Sequence 1303, App |
| 79 | 174 | 100.0 | 180 | 18 | US-10-775-204-1304 | Sequence 1304, App |
| 80 | 174 | 100.0 | 180 | 18 | US-10-775-204-1305 | Sequence 1305, App |
| 81 | 174 | 100.0 | 180 | 18 | US-10-775-204-1306 | Sequence 1306, App |
| 82 | 174 | 100.0 | 180 | 18 | US-10-775-204-1307 | Sequence 1307, App |
| 83 | 174 | 100.0 | 180 | 18 | US-10-775-204-1308 | Sequence 1308, App |
| 84 | 174 | 100.0 | 180 | 18 | US-10-775-204-1309 | Sequence 1309, App |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 14:54:46 ; Search time 52.5 Seconds

(without alignments)
52.610 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174

Sequence: 1 XXHADGFSDEMTILDNLAXRDFINWLIQTITDX 37

Scoring table:

BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 200 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 174 | 100.0 | 37 | 2 | US-08-669-790C-2 |
| 2 | 174 | 100.0 | 37 | 2 | US-08-422-540A-2 |
| 3 | 174 | 100.0 | 37 | 2 | US-08-422-540A-6 |
| 4 | 174 | 100.0 | 37 | 2 | US-08-422-540A-7 |
| 5 | 174 | 100.0 | 180 | 3 | US-08-784-582-56 |
| 6 | 174 | 100.0 | 180 | 3 | US-08-784-582-58 |
| 7 | 174 | 100.0 | 180 | 3 | US-08-784-582-61 |
| 8 | 174 | 100.0 | 360 | 3 | US-08-784-582-73 |
| 9 | 172 | 98.9 | 48 | 2 | US-08-808-825-8 |
| 10 | 170 | 97.7 | 33 | 1 | US-08-669-791C-2 |
| 11 | 170 | 97.7 | 33 | 2 | US-08-669-790C-3 |
| 12 | 170 | 97.7 | 33 | 2 | US-08-669-790C-4 |
| 13 | 170 | 97.7 | 33 | 2 | US-08-808-825-5 |
| 14 | 170 | 97.7 | 33 | 2 | US-08-808-825-6 |
| 15 | 170 | 97.7 | 33 | 2 | US-08-422-540A-3 |
| 16 | 170 | 97.7 | 33 | 3 | US-08-835-538C-2 |
| 17 | 170 | 97.7 | 33 | 3 | US-09-149-831-1 |
| 18 | 170 | 97.7 | 33 | 3 | US-09-149-831-2 |
| 19 | 170 | 97.7 | 33 | 4 | US-09-233-934-1 |
| 20 | 170 | 97.7 | 33 | 4 | US-09-233-934-2 |
| 21 | 170 | 97.7 | 33 | 4 | US-09-692-238-1 |
| 22 | 166 | 95.4 | 33 | 4 | US-09-692-238-2 |
| 23 | 162 | 92.1 | 33 | 2 | US-08-808-825-7 |
| 24 | 115 | 66.1 | 37 | 2 | US-08-422-540A-1 |
| 25 | 115 | 66.1 | 37 | 2 | US-08-422-540A-4 |
| 26 | 115 | 66.1 | 37 | 2 | US-08-422-540A-5 |
| 27 | 100 | 57.5 | 37 | 2 | US-08-669-790C-1 |

| | | | | | | |
|-----|----|------|----|---|------------------|--------------------|
| 28 | 85 | 48.9 | 35 | 2 | US-08-808-825-1 | Sequence 1, Appli |
| 29 | 80 | 46.0 | 38 | 3 | US-09-258-750-84 | Sequence 84, Appli |
| 30 | 80 | 46.0 | 38 | 4 | US-09-398-111-84 | Sequence 84, Appli |
| 31 | 80 | 46.0 | 39 | 3 | US-09-258-750-91 | Sequence 91, Appli |
| 32 | 80 | 46.0 | 39 | 4 | US-09-398-111-91 | Sequence 91, Appli |
| 33 | 78 | 44.8 | 31 | 3 | US-09-258-750-4 | Sequence 4, Appli |
| 34 | 78 | 44.8 | 31 | 3 | US-09-258-750-8 | Sequence 8, Appli |
| 35 | 78 | 44.8 | 31 | 4 | US-09-398-111-4 | Sequence 4, Appli |
| 36 | 78 | 44.8 | 31 | 4 | US-09-398-111-8 | Sequence 8, Appli |
| 37 | 78 | 44.8 | 32 | 3 | US-09-258-750-5 | Sequence 5, Appli |
| 38 | 78 | 44.8 | 32 | 3 | US-09-258-750-87 | Sequence 87, Appli |
| 39 | 78 | 44.8 | 32 | 4 | US-09-398-111-5 | Sequence 5, Appli |
| 40 | 78 | 44.8 | 32 | 4 | US-09-398-111-67 | Sequence 67, Appli |
| 41 | 78 | 44.8 | 33 | 3 | US-09-258-750-12 | Sequence 12, Appli |
| 42 | 78 | 44.8 | 33 | 3 | US-09-258-750-94 | Sequence 94, Appli |
| 43 | 78 | 44.8 | 33 | 4 | US-09-398-111-12 | Sequence 12, Appli |
| 44 | 78 | 44.8 | 33 | 4 | US-09-398-111-94 | Sequence 94, Appli |
| 45 | 78 | 44.8 | 34 | 3 | US-09-258-750-13 | Sequence 13, Appli |
| 46 | 78 | 44.8 | 34 | 4 | US-09-398-111-13 | Sequence 13, Appli |
| 47 | 77 | 44.3 | 34 | 3 | US-09-258-750-66 | Sequence 66, Appli |
| 48 | 77 | 44.3 | 34 | 4 | US-09-398-111-66 | Sequence 66, Appli |
| 49 | 77 | 44.3 | 35 | 3 | US-09-258-750-59 | Sequence 59, Appli |
| 50 | 77 | 44.3 | 35 | 3 | US-09-258-750-67 | Sequence 67, Appli |
| 51 | 77 | 44.3 | 35 | 4 | US-09-398-111-58 | Sequence 58, Appli |
| 52 | 77 | 44.3 | 35 | 4 | US-09-398-111-57 | Sequence 57, Appli |
| 53 | 77 | 44.3 | 36 | 3 | US-09-258-750-50 | Sequence 50, Appli |
| 54 | 77 | 44.3 | 36 | 3 | US-09-258-750-69 | Sequence 69, Appli |
| 55 | 77 | 44.3 | 36 | 3 | US-09-258-750-68 | Sequence 68, Appli |
| 56 | 77 | 44.3 | 36 | 4 | US-09-398-111-50 | Sequence 50, Appli |
| 57 | 77 | 44.3 | 36 | 4 | US-09-398-111-59 | Sequence 59, Appli |
| 58 | 77 | 44.3 | 36 | 4 | US-09-398-111-61 | Sequence 61, Appli |
| 59 | 77 | 44.3 | 37 | 3 | US-09-258-750-42 | Sequence 42, Appli |
| 60 | 77 | 44.3 | 37 | 3 | US-09-258-750-51 | Sequence 51, Appli |
| 61 | 77 | 44.3 | 37 | 3 | US-09-258-750-60 | Sequence 60, Appli |
| 62 | 77 | 44.3 | 37 | 3 | US-09-258-750-69 | Sequence 69, Appli |
| 63 | 77 | 44.3 | 37 | 4 | US-09-398-111-42 | Sequence 42, Appli |
| 64 | 77 | 44.3 | 37 | 4 | US-09-398-111-51 | Sequence 51, Appli |
| 65 | 77 | 44.3 | 37 | 4 | US-09-398-111-60 | Sequence 60, Appli |
| 66 | 77 | 44.3 | 37 | 4 | US-09-398-111-69 | Sequence 69, Appli |
| 67 | 77 | 44.3 | 38 | 3 | US-09-258-750-44 | Sequence 44, Appli |
| 68 | 77 | 44.3 | 38 | 3 | US-09-258-750-43 | Sequence 43, Appli |
| 69 | 77 | 44.3 | 38 | 3 | US-09-258-750-52 | Sequence 52, Appli |
| 70 | 77 | 44.3 | 38 | 3 | US-09-258-750-61 | Sequence 61, Appli |
| 71 | 77 | 44.3 | 38 | 3 | US-09-258-750-70 | Sequence 70, Appli |
| 72 | 77 | 44.3 | 38 | 3 | US-09-258-750-82 | Sequence 82, Appli |
| 73 | 77 | 44.3 | 38 | 4 | US-09-398-111-43 | Sequence 43, Appli |
| 74 | 77 | 44.3 | 38 | 4 | US-09-398-111-52 | Sequence 52, Appli |
| 75 | 77 | 44.3 | 38 | 4 | US-09-398-111-61 | Sequence 61, Appli |
| 76 | 77 | 44.3 | 38 | 4 | US-09-398-111-70 | Sequence 70, Appli |
| 77 | 77 | 44.3 | 38 | 4 | US-09-398-111-82 | Sequence 82, Appli |
| 78 | 77 | 44.3 | 39 | 3 | US-09-258-750-35 | Sequence 35, Appli |
| 79 | 77 | 44.3 | 39 | 3 | US-09-258-750-53 | Sequence 53, Appli |
| 80 | 77 | 44.3 | 39 | 3 | US-09-258-750-62 | Sequence 62, Appli |
| 81 | 77 | 44.3 | 39 | 3 | US-09-258-750-71 | Sequence 71, Appli |
| 82 | 77 | 44.3 | 39 | 3 | US-09-258-750-89 | Sequence 89, Appli |
| 83 | 77 | 44.3 | 39 | 3 | US-09-258-750-91 | Sequence 91, Appli |
| 84 | 77 | 44.3 | 39 | 4 | US-09-398-111-35 | Sequence 35, Appli |
| 85 | 77 | 44.3 | 39 | 4 | US-09-398-111-44 | Sequence 44, Appli |
| 86 | 77 | 44.3 | 39 | 4 | US-09-398-111-53 | Sequence 53, Appli |
| 87 | 77 | 44.3 | 39 | 4 | US-09-398-111-62 | Sequence 62, Appli |
| 88 | 77 | 44.3 | 39 | 4 | US-09-398-111-71 | Sequence 71, Appli |
| 89 | 77 | 44.3 | 39 | 4 | US-09-398-111-89 | Sequence 89, Appli |
| 90 | 77 | 44.3 | 39 | 4 | US-09-258-750-36 | Sequence 36, Appli |
| 91 | 77 | 44.3 | 40 | 3 | US-09-258-750-54 | Sequence 54, Appli |
| 92 | 77 | 44.3 | 40 | 3 | US-09-258-750-63 | Sequence 63, Appli |
| 93 | 77 | 44.3 | 40 | 3 | US-09-258-750-72 | Sequence 72, Appli |
| 94 | 77 | 44.3 | 40 | 3 | US-09-398-111-36 | Sequence 36, Appli |
| 95 | 77 | 44.3 | 40 | 4 | US-09-398-111-45 | Sequence 45, Appli |
| 96 | 77 | 44.3 | 40 | 4 | US-09-398-111-54 | Sequence 54, Appli |
| 97 | 77 | 44.3 | 40 | 4 | US-09-398-111-63 | Sequence 63, Appli |
| 98 | 77 | 44.3 | 40 | 4 | US-09-398-111-72 | Sequence 72, Appli |
| 99 | 77 | 44.3 | 40 | 4 | US-09-398-111-81 | Sequence 81, Appli |
| 100 | 77 | 44.3 | 40 | 4 | US-09-398-111-90 | Sequence 90, Appli |

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:43:07 ; Search time 56 Seconds

(without alignments)
255.538 Million cell updates/sec

Title: US-10-042-746-2

Sequence: 1 XXHADGSEFSDENMTILDNLAXRDFINMLIQKIDXX 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|-------------|
| 1 | 174 | 100.0 | 37 | ADP43244 | Rat/human |
| 2 | 174 | 100.0 | 180 | AAW16384 | Rat prepr |
| 3 | 174 | 100.0 | 180 | AAW22081 | Human pre |
| 4 | 174 | 100.0 | 180 | AAW22079 | Rat prepr |
| 5 | 174 | 100.0 | 180 | AAW22080 | Human pre |
| 6 | 174 | 100.0 | 180 | AAV39812 | Preproglu |
| 7 | 174 | 100.0 | 180 | AAW26773 | Rat prepr |
| 8 | 174 | 100.0 | 180 | AAW26774 | Human pre |
| 9 | 174 | 100.0 | 180 | AAW26775 | Mutant hu |
| 10 | 174 | 100.0 | 180 | ADP15331 | Human alb |
| 11 | 174 | 100.0 | 180 | ADP15334 | Human alb |
| 12 | 174 | 100.0 | 180 | ADP15335 | Human alb |
| 13 | 174 | 100.0 | 180 | ADP15336 | Human alb |
| 14 | 174 | 100.0 | 180 | ADP15337 | Human alb |
| 15 | 174 | 100.0 | 180 | ADP15338 | Human alb |
| 16 | 174 | 100.0 | 180 | ADP15339 | Human alb |
| 17 | 174 | 100.0 | 180 | ADP15340 | Human alb |
| 18 | 174 | 100.0 | 180 | ADP15341 | Human alb |
| 19 | 174 | 100.0 | 180 | ADP15342 | Human alb |
| 20 | 174 | 100.0 | 180 | ADP15343 | Human alb |
| 21 | 174 | 100.0 | 180 | ADP15344 | Human alb |
| 22 | 174 | 100.0 | 180 | ADP15345 | Human alb |
| 23 | 174 | 100.0 | 180 | ADP15346 | Human alb |
| 24 | 174 | 100.0 | 180 | ADP15347 | Human alb |
| 25 | 174 | 100.0 | 180 | ADP15348 | Human alb |

| | | | | | |
|----|-----|-------|-----|----------|-----------|
| 26 | 174 | 100.0 | 180 | ADH21630 | Human GLP |
| 27 | 174 | 100.0 | 180 | ADH21401 | Human GLP |
| 28 | 174 | 100.0 | 180 | ADH21402 | Human GLP |
| 29 | 174 | 100.0 | 180 | ADH21403 | Human GLP |
| 30 | 174 | 100.0 | 180 | ADH21632 | Human GLP |
| 31 | 174 | 100.0 | 180 | ADH21854 | Human GLP |
| 32 | 174 | 100.0 | 180 | ADH21629 | Human GLP |
| 33 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 34 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 35 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 36 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 37 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 38 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 39 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 40 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 41 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 42 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 43 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 44 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 45 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 46 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 47 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 48 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 49 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 50 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 51 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 52 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 53 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 54 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 55 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 56 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 57 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 58 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 59 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 60 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 61 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 62 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 63 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 64 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 65 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 66 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 67 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 68 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 69 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 70 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 71 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 72 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 73 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 74 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 75 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 76 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 77 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 78 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 79 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 80 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 81 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 82 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 83 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 84 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 85 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 86 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 87 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 88 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 89 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 90 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 91 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 92 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 93 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 94 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 95 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 96 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 97 | 174 | 100.0 | 180 | ADH21879 | Human GLP |
| 98 | 174 | 100.0 | 180 | ADH21879 | Human GLP |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds

(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPDEMTILDLNLRPFIMWLTQKTDXX 37

Scoring table: BIOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database :

1: PIR 79: *
2: Dirl: *
3: Dirl: *
4: Dirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 174 | 100.0 | 180 | 1 | GCGR |
| 2 | 174 | 100.0 | 180 | 1 | GCGR |
| 3 | 174 | 100.0 | 180 | 1 | GCGR |
| 4 | 169 | 97.1 | 180 | 1 | GCGR |
| 5 | 169 | 97.1 | 180 | 2 | AS7294 |
| 6 | 165 | 94.8 | 180 | 1 | GCGR |
| 7 | 164 | 94.3 | 158 | 1 | GCGR |
| 8 | 159 | 91.4 | 180 | 1 | GCGR |
| 9 | 115 | 66.1 | 206 | 2 | IS1301 |
| 10 | 90 | 51.7 | 101 | 1 | GCGR |
| 11 | 89 | 51.1 | 178 | 2 | IS1057 |
| 12 | 89 | 51.1 | 178 | 2 | IS1057 |
| 13 | 86 | 49.4 | 178 | 2 | IS1058 |
| 14 | 80 | 46.0 | 66 | 2 | IS1093 |
| 15 | 78 | 44.8 | 60 | 1 | GCGR |
| 16 | 77 | 44.3 | 29 | 2 | IS1093 |
| 17 | 76 | 43.7 | 30 | 2 | IS1093 |
| 18 | 76 | 43.7 | 63 | 1 | GCGR |
| 19 | 76 | 43.7 | 69 | 1 | GCGR |
| 20 | 76 | 43.7 | 122 | 1 | GCGR |
| 21 | 76 | 43.7 | 151 | 1 | GCGR |
| 22 | 75 | 43.1 | 29 | 1 | GCGR |
| 23 | 75 | 43.1 | 29 | 1 | GCGR |
| 24 | 74 | 42.5 | 72 | 1 | GCGR |
| 25 | 73 | 42.0 | 144 | 1 | GCGR |
| 26 | 72 | 41.4 | 153 | 1 | GCGR |
| 27 | 71 | 40.8 | 42 | 1 | GCGR |
| 28 | 71 | 40.8 | 42 | 1 | GCGR |
| 29 | 70 | 40.2 | 144 | 2 | IS1093 |

| | | | | | | |
|-----|------|------|------|---|------|--------------------|
| 30 | 69 | 39.7 | 29 | 1 | GCGR | glucagon - North A |
| 31 | 69 | 39.7 | 29 | 2 | GCGR | glucagon - turkey |
| 32 | 69 | 39.7 | 29 | 2 | GCGR | glucagon - common |
| 33 | 69 | 39.7 | 29 | 2 | GCGR | glucagon - Arabian |
| 34 | 69 | 39.7 | 29 | 2 | GCGR | glucagon - rabbit |
| 35 | 69 | 39.7 | 124 | 1 | GCGR | glucagon 1 precurs |
| 36 | 68 | 39.1 | 29 | 1 | GCGR | glucagon - ostrich |
| 37 | 68 | 39.1 | 29 | 1 | GCGR | glucagon - duck |
| 38 | 68 | 39.1 | 29 | 1 | GCGR | glucagon - slider |
| 39 | 67 | 38.5 | 29 | 2 | GCGR | glucagon - bowfin |
| 40 | 67 | 37.9 | 30 | 2 | GCGR | glucagon-like pept |
| 41 | 66 | 37.9 | 30 | 2 | GCGR | glucagon-like pept |
| 42 | 66 | 37.9 | 87 | 1 | GCGR | glucagon precursor |
| 43 | 64 | 36.8 | 29 | 1 | GCGR | glucagon - Europea |
| 44 | 64 | 36.8 | 29 | 2 | GCGR | glucagon - bigeye |
| 45 | 62 | 35.6 | 29 | 1 | GCGR | glucagon - Chinchi |
| 46 | 62 | 35.6 | 39 | 1 | GCGR | glucagon - Mexica |
| 47 | 62 | 35.6 | 2172 | 2 | GCGR | glucagon I - Europ |
| 48 | 61 | 35.1 | 29 | 2 | GCGR | glucagon I - Europ |
| 49 | 61 | 35.1 | 502 | 2 | GCGR | hypothetical prote |
| 50 | 59 | 33.9 | 850 | 2 | GCGR | hypothetical prote |
| 51 | 58 | 33.3 | 170 | 1 | GCGR | vasoactive intesti |
| 52 | 58 | 33.3 | 170 | 2 | GCGR | vasoactive intesti |
| 53 | 57 | 32.8 | 39 | 1 | GCGR | vasoactive intesti |
| 54 | 57 | 32.8 | 55 | 1 | GCGR | vasoactive intesti |
| 55 | 57 | 32.8 | 145 | 2 | GCGR | vasoactive intesti |
| 56 | 57 | 32.8 | 170 | 1 | GCGR | vasoactive intesti |
| 57 | 57 | 32.8 | 679 | 2 | GCGR | vasoactive intesti |
| 58 | 57 | 32.8 | 1260 | 2 | GCGR | hypothetical prote |
| 59 | 56 | 32.2 | 31 | 2 | GCGR | glucagon G2 - Nort |
| 60 | 55 | 31.6 | 55 | 1 | GCGR | vasoactive intesti |
| 61 | 55 | 31.6 | 58 | 1 | GCGR | vasoactive intesti |
| 62 | 55 | 31.6 | 765 | 2 | GCGR | hypothetical prote |
| 63 | 54.5 | 31.3 | 1088 | 2 | GCGR | glucagon G1 - Nort |
| 64 | 54 | 31.0 | 31 | 2 | GCGR | vasoactive intesti |
| 65 | 54 | 31.0 | 55 | 1 | GCGR | vasoactive intesti |
| 66 | 54 | 31.0 | 55 | 1 | GCGR | vasoactive intesti |
| 67 | 54 | 31.0 | 1075 | 1 | GCGR | heat-stable entero |
| 68 | 53.5 | 30.7 | 419 | 2 | GCGR | glycoprotein H pre |
| 69 | 53.5 | 30.7 | 808 | 1 | GCGR | hypothetical prote |
| 70 | 53 | 30.5 | 342 | 2 | GCGR | hypothetical prote |
| 71 | 53 | 30.5 | 464 | 2 | GCGR | thiophene and fura |
| 72 | 53 | 30.5 | 494 | 2 | GCGR | conserved hypothet |
| 73 | 52.5 | 30.2 | 79 | 2 | GCGR | hypothetical prote |
| 74 | 52.5 | 30.2 | 460 | 2 | GCGR | argininosuccinate |
| 75 | 52.5 | 30.2 | 1151 | 2 | GCGR | hypothetical prote |
| 76 | 52 | 29.9 | 36 | 2 | GCGR | glucagon II - Euro |
| 77 | 52 | 29.9 | 298 | 2 | GCGR | hypothetical prote |
| 78 | 52 | 29.9 | 344 | 2 | GCGR | hypothetical prote |
| 79 | 52 | 29.9 | 388 | 2 | GCGR | hypothetical prote |
| 80 | 52 | 29.9 | 512 | 2 | GCGR | IS3 family transpo |
| 81 | 52 | 29.9 | 512 | 2 | GCGR | IS3 family transpo |
| 82 | 52 | 29.9 | 512 | 2 | GCGR | IS3 family transpo |
| 83 | 52 | 29.9 | 512 | 2 | GCGR | probable transpos |
| 84 | 52 | 29.9 | 512 | 2 | GCGR | probable transpos |
| 85 | 52 | 29.9 | 512 | 2 | GCGR | ATPase component o |
| 86 | 52 | 29.9 | 648 | 2 | GCGR | hypothetical prote |
| 87 | 52 | 29.9 | 1077 | 2 | GCGR | hypothetical prote |
| 88 | 51.5 | 29.6 | 1999 | 2 | GCGR | neuropeptides prec |
| 89 | 51 | 29.3 | 173 | 2 | GCGR | conserved hypothet |
| 90 | 51 | 29.3 | 333 | 2 | GCGR | hypothetical prote |
| 91 | 51 | 29.3 | 335 | 2 | GCGR | conserved hypothet |
| 92 | 51 | 29.3 | 336 | 2 | GCGR | unknown protein en |
| 93 | 51 | 29.3 | 349 | 2 | GCGR | hypothetical prote |
| 94 | 51 | 29.3 | 349 | 2 | GCGR | hypothetical prote |
| 95 | 51 | 29.3 | 349 | 2 | GCGR | hypothetical prote |
| 96 | 51 | 29.3 | 349 | 2 | GCGR | hypothetical prote |
| 97 | 51 | 29.3 | 662 | 2 | GCGR | hypothetical prote |
| 98 | 51 | 29.3 | 990 | 2 | GCGR | hypothetical prote |
| 99 | 51 | 29.3 | 1007 | 2 | GCGR | disease resistance |
| 100 | 50.5 | 29.0 | 165 | 2 | GCGR | probable bacteriop |
| 101 | 50.5 | 29.0 | 1369 | 2 | GCGR | hypothetical prote |
| 102 | 50.5 | 29.0 | 1600 | 2 | GCGR | glutamate dehydrog |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:03:46 : Search time 199.5 Seconds

(without alignments)
94.972 Million cell updates/sec

Title: US-10-042-746-2

Perfect score: 174
Sequence: 1 XXHADGSPFEDENITLNLAXRPFINMLIQTITDX 37

Scoring table: BLOSUM62X
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 174 | 100.0 | 180 | 1 | GLUC_CAVPO |
| 2 | 174 | 100.0 | 180 | 1 | GLUC_HUMAN |
| 3 | 174 | 100.0 | 180 | 1 | GLUC_RAT |
| 4 | 169 | 97.1 | 80 | 2 | Q6IUP8 |
| 5 | 169 | 97.1 | 180 | 1 | GLUC_MESAU |
| 6 | 169 | 97.1 | 180 | 1 | GLUC_MOUSE |
| 7 | 166 | 95.4 | 180 | 1 | GLUC_BOVIN |
| 8 | 166 | 95.4 | 180 | 1 | GLUC_PIG |
| 9 | 165 | 94.8 | 180 | 1 | GLUC_CANPA |
| 10 | 165 | 94.8 | 180 | 1 | GLUC_OCTDR |
| 11 | 153 | 87.9 | 176 | 1 | GLUC_SHEEP |
| 12 | 115 | 66.1 | 206 | 1 | GLUC_CHICK |
| 13 | 109 | 62.6 | 266 | 2 | Q6D1Z4 |
| 14 | 105 | 60.3 | 145 | 2 | Q6RYB5 |
| 15 | 104 | 59.8 | 124 | 2 | Q6RYB1 |
| 16 | 104 | 59.8 | 170 | 2 | Q6RYB4 |
| 17 | 104 | 59.8 | 204 | 1 | GLUC_HELISU |
| 18 | 103 | 59.2 | 266 | 1 | GLUI_XENLA |
| 19 | 99 | 56.9 | 153 | 2 | Q6RYB6 |
| 20 | 92 | 52.9 | 149 | 2 | Q6RYB2 |
| 21 | 92 | 52.9 | 220 | 2 | Q6RYB3 |
| 22 | 91 | 52.3 | 120 | 1 | GLU2_PETMA |
| 23 | 90 | 51.7 | 103 | 1 | GLU1_PETMA |
| 24 | 90 | 51.7 | 160 | 1 | GLU1_PETMA |
| 25 | 89 | 51.1 | 178 | 1 | GLU1_ONCMY |
| 26 | 89 | 51.1 | 178 | 1 | GLU2_ONCMY |
| 27 | 88 | 50.6 | 173 | 2 | Q6RYB3 |
| 28 | 87 | 50.0 | 173 | 2 | Q6RYB9 |
| 29 | 86 | 49.4 | 36 | 1 | GLUC_HYDCO |
| 30 | 86 | 49.4 | 176 | 2 | Q6RYB0 |
| 31 | 86 | 49.4 | 176 | 2 | Q6RYC2 |

| | | | | | | |
|-----|------|------|------|---|-------------|---------------------|
| 32 | 80 | 46.0 | 62 | 1 | GLUC_SCYCA | P09687 bcyliothinu |
| 33 | 80 | 46.0 | 66 | 2 | Q788W6 | Q788W6 oncorhynch |
| 34 | 80 | 46.0 | 72 | 2 | Q91409 | Q91409 oncorhynch |
| 35 | 79 | 45.4 | 122 | 2 | Q6RYB8 | Q6RYB8 ictalurus p |
| 36 | 78 | 44.8 | 68 | 1 | GLUC_ONCK1 | P07449 oncorhynch |
| 37 | 78 | 44.8 | 219 | 1 | GLU2_XENLA | Q42144 xenopus lae |
| 38 | 77 | 44.3 | 29 | 1 | GLUC_TORRA | P09567 toipede mar |
| 39 | 76 | 43.7 | 30 | 2 | Q7LZB3 | Q7LZB3 polyodon sp |
| 40 | 76 | 43.7 | 122 | 1 | GLU2_IOPAM | P04092 lophius ame |
| 41 | 75 | 43.1 | 29 | 1 | GLUC_CALMI | P13189 callorhynch |
| 42 | 75 | 43.1 | 71 | 1 | GLUC_ICTPU | P04093 ictalurus p |
| 43 | 75 | 43.1 | 71 | 1 | GLUC_P1AME | P81880 piactetus m |
| 44 | 74 | 42.5 | 45 | 2 | Q6PPF4 | Q6PPF4 capra hircu |
| 45 | 74 | 42.5 | 78 | 1 | GLUC_LEPSP | Q6RYB7 ictalurus p |
| 46 | 74 | 42.5 | 120 | 2 | Q6RYB7 | P79695 carassius a |
| 47 | 73 | 42.0 | 121 | 1 | GLUC_CARAU | Q66145 rattus norv |
| 48 | 73 | 42.0 | 144 | 1 | GIP_RAT | Q6RYC1 sebaestes ca |
| 49 | 72 | 41.4 | 121 | 2 | Q6RYC1 | Q66145 sebaestes ca |
| 50 | 72 | 41.4 | 121 | 2 | Q6RYC1 | Q66145 sebaestes ca |
| 51 | 72 | 41.4 | 153 | 1 | GIP_HUMAN | Q66145 sebaestes ca |
| 52 | 72 | 41.4 | 153 | 2 | Q6NTD3 | Q66145 sebaestes ca |
| 53 | 71 | 40.8 | 36 | 1 | GLU1_ORENT | Q66145 sebaestes ca |
| 54 | 71 | 40.8 | 42 | 1 | GIP_BOVIN | Q66145 sebaestes ca |
| 55 | 71 | 40.8 | 42 | 1 | GIP_PIG | Q66145 sebaestes ca |
| 56 | 70 | 40.2 | 29 | 1 | GLUC_CAMP | Q66145 sebaestes ca |
| 57 | 70 | 40.2 | 130 | 2 | Q6CVF1 | Q66145 sebaestes ca |
| 58 | 70 | 40.2 | 144 | 2 | GIP_MOUSE | Q66145 sebaestes ca |
| 59 | 70 | 40.2 | 144 | 2 | Q9D887 | Q66145 sebaestes ca |
| 60 | 70 | 40.2 | 500 | 2 | Q649W5 | Q66145 sebaestes ca |
| 61 | 69 | 39.7 | 29 | 1 | GLUC_CAMP | Q66145 sebaestes ca |
| 62 | 69 | 39.7 | 29 | 1 | GLUC_DIDMA | Q66145 sebaestes ca |
| 63 | 69 | 39.7 | 29 | 1 | GLUC_MELGA | Q66145 sebaestes ca |
| 64 | 69 | 39.7 | 29 | 1 | GLUC_RABIT | Q66145 sebaestes ca |
| 65 | 69 | 39.7 | 29 | 1 | GLUC_SALIC | Q66145 sebaestes ca |
| 66 | 69 | 39.7 | 123 | 2 | Q6RYA9 | Q66145 sebaestes ca |
| 67 | 69 | 39.7 | 124 | 1 | GLU1_LOPM | Q66145 sebaestes ca |
| 68 | 68 | 39.1 | 29 | 1 | GLUC_AMP | Q66145 sebaestes ca |
| 69 | 67 | 38.5 | 96 | 2 | Q6D43 | Q66145 sebaestes ca |
| 70 | 67 | 38.5 | 96 | 2 | Q6D43 | Q66145 sebaestes ca |
| 71 | 66 | 37.9 | 30 | 1 | GLUM_ANGRO | Q66145 sebaestes ca |
| 72 | 66 | 37.9 | 30 | 1 | GLUC_ANGRO | Q66145 sebaestes ca |
| 73 | 66 | 37.9 | 96 | 1 | GLUC_MYOSC | Q66145 sebaestes ca |
| 74 | 64 | 36.8 | 29 | 1 | GLUC_PLARE | Q66145 sebaestes ca |
| 75 | 64 | 36.8 | 87 | 2 | Q7SZU6 | Q66145 sebaestes ca |
| 76 | 62 | 35.6 | 29 | 1 | GLUC_CHIR | Q66145 sebaestes ca |
| 77 | 62 | 35.6 | 39 | 1 | EXB3_HELMO | Q66145 sebaestes ca |
| 78 | 62 | 35.6 | 2162 | 2 | Q6RYA5 | Q66145 sebaestes ca |
| 79 | 61.5 | 35.3 | 145 | 2 | Q7NIM1 | Q66145 sebaestes ca |
| 80 | 61 | 35.1 | 502 | 2 | Q6RS41 | Q66145 sebaestes ca |
| 81 | 60 | 34.5 | 170 | 1 | VIP_BOVIN | Q66145 sebaestes ca |
| 82 | 60 | 34.5 | 626 | 2 | Q6OWG7 | Q66145 sebaestes ca |
| 83 | 59.5 | 34.2 | 2980 | 2 | Q6IAK3 | Q66145 sebaestes ca |
| 84 | 59 | 33.9 | 87 | 1 | EXB4_HELISU | Q66145 sebaestes ca |
| 85 | 59 | 33.9 | 200 | 1 | VIP_CHICK | Q66145 sebaestes ca |
| 86 | 59 | 33.9 | 387 | 2 | Q6FSR2 | Q66145 sebaestes ca |
| 87 | 59 | 33.9 | 850 | 2 | Q6FLF5 | Q66145 sebaestes ca |
| 88 | 58 | 33.3 | 153 | 2 | Q7TSR4 | Q66145 sebaestes ca |
| 89 | 58 | 33.3 | 170 | 1 | VIP_MOUSE | Q66145 sebaestes ca |
| 90 | 58 | 33.3 | 170 | 1 | VIP_RAT | Q66145 sebaestes ca |
| 91 | 58 | 33.3 | 171 | 2 | Q6D2Z7 | Q66145 sebaestes ca |
| 92 | 58 | 33.3 | 175 | 1 | PACA_CHICK | Q66145 sebaestes ca |
| 93 | 58 | 33.3 | 200 | 1 | VIP_MELGA | Q66145 sebaestes ca |
| 94 | 57 | 32.8 | 145 | 2 | Q7M2Y9 | Q66145 sebaestes ca |
| 95 | 57 | 32.8 | 170 | 1 | VIP_HUMAN | Q66145 sebaestes ca |
| 96 | 57 | 32.8 | 679 | 2 | Q7ZV68 | Q66145 sebaestes ca |
| 97 | 57 | 32.8 | 679 | 2 | Q23352 | Q66145 sebaestes ca |
| 98 | 57 | 32.8 | 787 | 2 | Q64C98 | Q66145 sebaestes ca |
| 99 | 57 | 32.8 | 1260 | 2 | Q61307 | Q66145 sebaestes ca |
| 100 | 56.5 | 32.5 | 559 | 2 | Q6ZMP5 | Q66145 sebaestes ca |
| 101 | 56.5 | 32.5 | 608 | 2 | Q6CTU0 | Q66145 sebaestes ca |
| 102 | 56 | 32.2 | 31 | 2 | Q7LZB2 | Q66145 sebaestes ca |
| 103 | 56 | 32.2 | 1128 | 2 | Q7T512 | Q66145 sebaestes ca |
| 104 | 56 | 32.2 | 73 | 1 | VIP_HUMAN | Q66145 sebaestes ca |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds
(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-2

Sequence: 174
1 XXHADSGFSDENNTIIDNLAXRDPINWLTQTKITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : PIR 79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 174 | 100.0 | 180 | 1 GCGP | glucagon precursor |
| 2 | 174 | 100.0 | 180 | 1 GCHU | glucagon precursor |
| 3 | 174 | 100.0 | 180 | 1 GCHU | glucagon precursor |
| 4 | 169 | 97.1 | 180 | 1 GCHV | glucagon precursor |
| 5 | 169 | 97.1 | 180 | 2 A57294 | glucagon precursor |
| 6 | 165 | 94.8 | 180 | 1 GCRDU | glucagon precursor |
| 7 | 164 | 94.3 | 158 | 1 GCPG | glucagon precursor |
| 8 | 159 | 91.4 | 180 | 1 GCHO | glucagon precursor |
| 9 | 115 | 66.1 | 206 | 2 I51301 | proglucagon - chic |
| 10 | 90 | 51.7 | 101 | 1 GCRB | glucagon precursor |
| 11 | 89 | 51.1 | 178 | 2 I51057 | glucagon II precurs |
| 12 | 86 | 49.4 | 178 | 2 I51058 | glucagon I precurs |
| 13 | 86 | 49.4 | 36 | 1 GCFI | glucagon-36 - spot |
| 14 | 80 | 46.0 | 66 | 2 I51093 | glucagon - chinook |
| 15 | 78 | 44.8 | 60 | 1 GCONC | glucagon precursor |
| 16 | 77 | 44.3 | 29 | 2 S07211 | glucagon - marbled |
| 17 | 76 | 43.7 | 30 | 2 S44473 | glucagon-like pept |
| 18 | 76 | 43.7 | 63 | 1 GCIDC | glucagon precursor |
| 19 | 76 | 43.7 | 69 | 1 GCDG69 | glucagon-69 - dog |
| 20 | 76 | 43.7 | 122 | 1 GCAF2 | glucagon 2 precurs |
| 21 | 76 | 43.7 | 151 | 1 GCGH | glucagon precursor |
| 22 | 75 | 43.1 | 29 | 1 GCDP | glucagon - smaller |
| 23 | 75 | 43.1 | 29 | 1 GCEN | glucagon - elephant |
| 24 | 74 | 42.5 | 72 | 1 GCGXA | glucagon precursor |
| 25 | 73 | 42.0 | 144 | 1 JN0589 | glucoside-dependent |
| 26 | 72 | 41.4 | 153 | 1 A28406 | gastric inhibitory |
| 27 | 71 | 40.8 | 42 | 1 GIBO | gastric inhibitory |
| 28 | 71 | 40.8 | 42 | 1 GIPG | gastric inhibitory |
| 29 | 70 | 40.2 | 144 | 2 S71426 | glucose-dependent |

| | | | | | |
|-----|------|------|------|-----------|---------------------|
| 30 | 69 | 39.7 | 29 | 1 GCOV | glucagon - North A |
| 31 | 69 | 39.7 | 29 | 2 A91740 | glucagon - turkey |
| 32 | 69 | 39.7 | 29 | 2 C39258 | glucagon - common |
| 33 | 69 | 39.7 | 29 | 2 A91742 | glucagon - Arabian |
| 34 | 69 | 39.7 | 29 | 2 A91741 | glucagon - rabbit |
| 35 | 69 | 39.7 | 124 | 1 GCAF | glucagon 1 precurs |
| 36 | 68 | 39.1 | 29 | 1 A61583 | glucagon - ostrich |
| 37 | 68 | 39.1 | 29 | 1 GCDK | glucagon - duck |
| 38 | 68 | 39.1 | 29 | 1 GCCT | glucagon - slider |
| 39 | 67 | 38.5 | 29 | 2 S39018 | glucagon - bowfin |
| 40 | 66 | 37.9 | 30 | 2 C61125 | glucagon-like pept |
| 41 | 66 | 37.9 | 30 | 2 B61125 | glucagon-like pept |
| 42 | 66 | 37.9 | 87 | 1 GCFIS | glucagon precursor |
| 43 | 64 | 36.8 | 29 | 1 GCFIS | glucagon - Europea |
| 44 | 64 | 36.8 | 29 | 2 A61135 | glucagon - bigeye |
| 45 | 62 | 35.6 | 29 | 1 GCCB | glucagon - Chinchi |
| 46 | 62 | 35.6 | 39 | 1 HMG32 | extensin-3 - Mexica |
| 47 | 62 | 35.6 | 2172 | 2 T20145 | hypothetical prote |
| 48 | 61 | 35.1 | 29 | 2 C60840 | glucagon I - Europ |
| 49 | 61 | 35.1 | 502 | 2 H75290 | hypothetical prote |
| 50 | 59 | 33.9 | 82 | 2 H75290 | hypothetical prote |
| 51 | 58 | 33.3 | 170 | 1 VRR | vasoactive intesti |
| 52 | 58 | 33.3 | 170 | 2 A60037 | vasoactive intesti |
| 53 | 57 | 32.8 | 39 | 1 HMG4G | extensin-4 - Gila m |
| 54 | 57 | 32.8 | 55 | 1 VRGP | vasoactive intesti |
| 55 | 57 | 32.8 | 145 | 2 A60038 | vasoactive intesti |
| 56 | 57 | 32.8 | 170 | 1 VRHU | vasoactive intesti |
| 57 | 57 | 32.8 | 679 | 2 C71413 | hypothetical prote |
| 58 | 57 | 32.8 | 1260 | 2 T01334 | hypothetical prote |
| 59 | 56 | 32.2 | 31 | 2 S44472 | glucagon G2 - Nort |
| 60 | 55 | 31.6 | 55 | 1 VRB | vasoactive intesti |
| 61 | 55 | 31.6 | 58 | 1 VRP | vasoactive intesti |
| 62 | 55 | 31.6 | 765 | 2 G64228 | hypothetical prote |
| 63 | 54.5 | 31.0 | 1088 | 2 C83054 | hypothetical prote |
| 64 | 54 | 31.0 | 31 | 2 S44471 | glucagon G1 - Nort |
| 65 | 54 | 31.0 | 55 | 1 VRBO | vasoactive intesti |
| 66 | 54 | 31.0 | 55 | 1 VRSH | vasoactive intesti |
| 67 | 54 | 31.0 | 1075 | 1 OYRTX | heat-stable entero |
| 68 | 53.5 | 30.7 | 419 | 2 S74329 | hypothetical prote |
| 69 | 53.5 | 30.7 | 808 | 1 JQ02043 | glycoprotein H pre |
| 70 | 53 | 30.5 | 342 | 2 T16444 | hypothetical prote |
| 71 | 53 | 30.5 | 464 | 2 D82375 | hypothetical prote |
| 72 | 53 | 30.5 | 494 | 2 B82874 | thiophene and fura |
| 73 | 52.5 | 30.2 | 79 | 2 AB1982 | conserved hypothet |
| 74 | 52.5 | 30.2 | 460 | 2 T39462 | hypothetical prote |
| 75 | 52.5 | 30.2 | 1151 | 2 T24541 | hypothetical prote |
| 76 | 52 | 29.9 | 36 | 2 D60840 | glucagon II - Euro |
| 77 | 52 | 29.9 | 298 | 2 F69502 | hypothetical prote |
| 78 | 52 | 29.9 | 344 | 2 S64931 | hypothetical prote |
| 79 | 52 | 29.9 | 388 | 2 H64427 | hypothetical prote |
| 80 | 52 | 29.9 | 512 | 2 AC3203 | IS3 family transpo |
| 81 | 52 | 29.9 | 512 | 2 AD2835 | IS3 family transpo |
| 82 | 52 | 29.9 | 512 | 2 AD3049 | IS3 family transpo |
| 83 | 52 | 29.9 | 512 | 2 G97612 | probable transposa |
| 84 | 52 | 29.9 | 512 | 2 G98236 | probable transposa |
| 85 | 52 | 29.9 | 518 | 2 D97310 | ATPase component o |
| 86 | 52 | 29.9 | 648 | 2 T09036 | hypothetical prote |
| 87 | 52 | 29.9 | 1077 | 2 S66842 | hypothetical prote |
| 88 | 51.5 | 29.6 | 1999 | 2 AB2018 | hypothetical prote |
| 89 | 51 | 29.3 | 173 | 2 S34767 | neuropeptides prec |
| 90 | 51 | 29.3 | 333 | 2 B83288 | conserved hypothet |
| 91 | 51 | 29.3 | 335 | 2 B90764 | hypothetical prote |
| 92 | 51 | 29.3 | 336 | 2 B70102 | conserved hypothet |
| 93 | 51 | 29.3 | 349 | 2 D85678 | unknown protein en |
| 94 | 51 | 29.3 | 349 | 2 H85626 | hypothetical prote |
| 95 | 51 | 29.3 | 349 | 2 B90819 | hypothetical prote |
| 96 | 51 | 29.3 | 349 | 2 B90912 | hypothetical prote |
| 97 | 51 | 29.3 | 662 | 2 T33900 | hypothetical prote |
| 98 | 51 | 29.3 | 990 | 2 T05197 | hypothetical prote |
| 99 | 51 | 29.3 | 1007 | 2 G96606 | disease resistance |
| 100 | 50.5 | 29.0 | 165 | 2 AG0619 | probable bacteriop |
| 101 | 50.5 | 29.0 | 1369 | 2 T32338 | hypothetical prote |
| 102 | 50.5 | 29.0 | 1600 | 2 AB3281 | glutamate dehydrog |

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CM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:17:30 ; Search time 490 Seconds

(without alignments)
529.404 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155

Sequence: 1 XXHADGFSFSDMTXLDLXAXDFINWLXXTKITDXX 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 8766186 seqs, 3505510206 residues

Total number of hits satisfying chosen parameters: 17532372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Command line parameters:
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-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -NATRIX=blsuns2DX
-TRANS=human40.cdi -LIST=200 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=125 -MODB=LOCAL -OUTFMT=ptco -NORM=ext -HABSIZE=500
-MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 @cgn 1 1 582 @runat 17102005_100128_4884 -NCPU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 155 | 100.0 | 449 | 14 | US-10-060-036-3474 Sequence 3477, Ap |
| 2 | 155 | 100.0 | 449 | 14 | US-10-060-036-4108 Sequence 4108, Ap |
| 3 | 155 | 100.0 | 517 | 14 | US-10-060-036-3938 Sequence 3938, Ap |
| 4 | 155 | 100.0 | 543 | 21 | US-10-775-180-60 Sequence 60, Appl |
| 5 | 155 | 100.0 | 543 | 21 | US-10-775-180-61 Sequence 61, Appl |
| 6 | 155 | 100.0 | 543 | 21 | US-10-775-180-62 Sequence 62, Appl |
| 7 | 155 | 100.0 | 543 | 21 | US-10-775-180-63 Sequence 63, Appl |
| 8 | 155 | 100.0 | 543 | 21 | US-10-775-180-412 Sequence 412, Ap |
| 9 | 155 | 100.0 | 543 | 21 | US-10-775-180-413 Sequence 413, Ap |
| 10 | 155 | 100.0 | 543 | 21 | US-10-775-180-414 Sequence 414, Ap |
| 11 | 155 | 100.0 | 543 | 21 | US-10-775-180-415 Sequence 415, Appl |
| 12 | 155 | 100.0 | 543 | 21 | US-10-775-180-416 Sequence 416, Appl |
| 13 | 155 | 100.0 | 543 | 21 | US-10-775-180-499 Sequence 499, Ap |
| 14 | 155 | 100.0 | 543 | 21 | US-10-775-180-523 Sequence 523, Ap |
| 15 | 155 | 100.0 | 543 | 21 | US-10-775-180-524 Sequence 524, Ap |
| 16 | 155 | 100.0 | 543 | 21 | US-10-775-204-198 Sequence 198, Ap |
| 17 | 155 | 100.0 | 543 | 22 | US-10-775-204-200 Sequence 200, Ap |
| 18 | 155 | 100.0 | 543 | 22 | US-10-775-204-201 Sequence 201, Ap |
| 19 | 155 | 100.0 | 543 | 22 | US-10-775-204-202 Sequence 202, Ap |
| 20 | 155 | 100.0 | 543 | 22 | US-10-775-204-1216 Sequence 1216, Ap |
| 21 | 155 | 100.0 | 543 | 22 | US-10-775-204-1217 Sequence 1217, Ap |
| 22 | 155 | 100.0 | 543 | 22 | US-10-775-204-1218 Sequence 1218, Ap |
| 23 | 155 | 100.0 | 543 | 22 | US-10-775-204-1219 Sequence 1219, Ap |
| 24 | 155 | 100.0 | 543 | 22 | US-10-775-204-1230 Sequence 1220, Ap |
| 25 | 155 | 100.0 | 543 | 22 | US-10-775-204-1391 Sequence 1391, Ap |
| 26 | 155 | 100.0 | 543 | 22 | US-10-775-204-1439 Sequence 1439, Ap |
| 27 | 155 | 100.0 | 543 | 22 | US-10-775-204-1440 Sequence 1440, Ap |
| 28 | 155 | 100.0 | 673 | 14 | US-10-060-036-4237 Ap |
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 16, 2005, 20:52:27 ; Search time 123.5 Seconds

(without alignments)
490.221 Million cell updates/sec

Title: us-10-042-746-1

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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Tue Oct 18 16:18:17 2005

us-10-042-746-1.rng

Page 1

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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)

586,427 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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| 56 | 155 | 100.0 | 543 | 10 | ADP16142 | Adf16142 Human alb |
| 57 | 155 | 100.0 | 543 | 10 | ADP16141 | Adf16141 Human alb |
| 58 | 155 | 100.0 | 543 | 10 | ADP16140 | Adf16140 Human alb |
| 59 | 155 | 100.0 | 543 | 10 | ADP16139 | Adf16139 Human alb |
| 60 | 155 | 100.0 | 543 | 10 | ADP16138 | Adf16138 Human alb |
| 61 | 155 | 100.0 | 543 | 10 | ADP16137 | Adf16137 Human alb |
| 62 | 155 | 100.0 | 543 | 10 | ADP16136 | Adf16136 Human alb |
| 63 | 155 | 100.0 | 543 | 10 | ADP16135 | Adf16135 Human alb |
| 64 | 155 | 100.0 | 543 | 10 | ADP16134 | Adf16134 Human alb |
| 65 | 155 | 100.0 | 543 | 10 | ADP16133 | Adf16133 Human alb |
| 66 | 155 | 100.0 | 543 | 10 | ADP16132 | Adf16132 Human alb |
| 67 | 155 | 100.0 | 543 | 10 | ADP16131 | Adf16131 Human alb |
| 68 | 155 | 100.0 | 543 | 10 | ADP16130 | Adf16130 Human alb |
| 69 | 155 | 100.0 | 543 | 10 | ADP16129 | Adf16129 Human alb |
| 70 | 155 | 100.0 | 543 | 10 | ADP16128 | Adf16128 Human alb |
| 71 | 155 | 100.0 | 543 | 10 | ADP16127 | Adf16127 Human alb |
| 72 | 155 | 100.0 | 543 | 10 | ADP16126 | Adf16126 Human alb |
| 73 | 155 | 100.0 | 543 | 10 | ADP16125 | Adf16125 Human alb |
| 74 | 155 | 100.0 | 543 | 10 | ADP16124 | Adf16124 Human alb |
| 75 | 155 | 100.0 | 543 | 10 | ADP16123 | Adf16123 Human alb |
| 76 | 155 | 100.0 | 543 | 10 | ADP16122 | Adf16122 Human alb |
| 77 | 155 | 100.0 | 543 | 10 | ADP16121 | Adf16121 Human alb |
| 78 | 155 | 100.0 | 543 | 10 | ADP16120 | Adf16120 Human alb |

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 17:08:30 ; Search time 2836.5 Seconds

(without alignments)
632.062 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XHHADGFSDEMTXLDLXKXPFIMWLXXTKITDXK 37

Scoring table:

BLOSUM62DX
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%
Listing first 200 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xjh
-Q=/cgn2.1/USPTO.spool/US10042746/runat.17102005.100127.4844/app.query.fasta.1.398
-DB=GenBml -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LIST=200
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62DX -TRANS=human40.cdi -LST=200
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=125 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HSPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US10042746.@CGN.1.1.3851.@runat.17102005.100127.4844 -NCPU=6 -ICPU=3
-NO MMAP -LARGEDUTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 155 | 100.0 | 241 | 10 | AY623893 Phodopus |
| 2 | 155 | 100.0 | 243 | 10 | RATGLUS |
| 3 | 155 | 100.0 | 543 | 9 | BT006813 |
| 4 | 155 | 100.0 | 543 | 12 | BT007507 |

| | | | | | |
|----|-----|-------|--------|----|---------------------|
| 5 | 155 | 100.0 | 574 | 4 | AY242124 Sus scrofa |
| 6 | 155 | 100.0 | 895 | 6 | AR108106 |
| 7 | 155 | 100.0 | 955 | 6 | AR108107 |
| 8 | 155 | 100.0 | 955 | 6 | AR108109 |
| 9 | 155 | 100.0 | 1034 | 6 | A31421 |
| 10 | 155 | 100.0 | 1036 | 6 | CQ729100 |
| 11 | 155 | 100.0 | 1053 | 10 | GP1G |
| 12 | 155 | 100.0 | 1062 | 6 | AR270649 |
| 13 | 155 | 100.0 | 1062 | 9 | HUMGLUC |
| 14 | 155 | 100.0 | 1104 | 10 | OCOCGLU |
| 15 | 155 | 100.0 | 1108 | 4 | BOVGG |
| 16 | 155 | 100.0 | 1118 | 10 | HAMGG |
| 17 | 155 | 100.0 | 1123 | 4 | AF308439 |
| 18 | 155 | 100.0 | 1154 | 9 | BC005278 |
| 19 | 155 | 100.0 | 2356 | 6 | AR108119 |
| 20 | 155 | 100.0 | 3798 | 6 | CQ493428 |
| 21 | 155 | 100.0 | 4146 | 6 | CQ414344 |
| 22 | 155 | 100.0 | 6455 | 9 | HSGJUC |
| 23 | 155 | 100.0 | 10050 | 9 | HSGJUC2 |
| 24 | 155 | 100.0 | 163681 | 9 | AC007750 |
| 25 | 155 | 100.0 | 223513 | 2 | AC111919 |
| 26 | 155 | 100.0 | 223513 | 2 | AC097841 |
| 27 | 154 | 99.4 | 145 | 6 | CQ054796 |
| 28 | 154 | 99.4 | 145 | 6 | CQ074034 |
| 29 | 154 | 99.4 | 145 | 6 | CQ104933 |
| 30 | 154 | 99.4 | 145 | 6 | CQ143637 |
| 31 | 154 | 99.4 | 145 | 6 | CQ179117 |
| 32 | 154 | 99.4 | 145 | 6 | CQ203473 |
| 33 | 154 | 99.4 | 145 | 6 | CQ226837 |
| 34 | 154 | 99.4 | 145 | 6 | CQ264982 |
| 35 | 154 | 99.4 | 145 | 6 | CQ302070 |
| 36 | 154 | 99.4 | 145 | 6 | CQ339262 |
| 37 | 150 | 96.8 | 668 | 10 | MMPROGLG |
| 38 | 150 | 96.8 | 1102 | 10 | BC012975 |
| 39 | 150 | 96.8 | 1116 | 10 | AF276754 |
| 40 | 150 | 96.8 | 188169 | 10 | AL928876 |
| 41 | 150 | 96.8 | 209762 | 2 | AC115074 |
| 42 | 150 | 96.8 | 219014 | 2 | AC024141 |
| 43 | 142 | 91.6 | 559 | 4 | AX147453 |
| 44 | 142 | 91.6 | 1056 | 6 | AX147453 |
| 45 | 109 | 70.3 | 1186 | 5 | S78477 |
| 46 | 109 | 70.3 | 1360 | 5 | BC075391 |
| 47 | 105 | 67.7 | 360 | 6 | CQ064797 |
| 48 | 105 | 67.7 | 360 | 6 | CQ091744 |
| 49 | 105 | 67.7 | 360 | 6 | CQ130570 |
| 50 | 105 | 67.7 | 360 | 6 | CQ169179 |
| 51 | 105 | 67.7 | 360 | 6 | CQ198311 |
| 52 | 105 | 67.7 | 360 | 6 | CQ213772 |
| 53 | 105 | 67.7 | 360 | 6 | CQ252355 |
| 54 | 105 | 67.7 | 360 | 6 | CQ289502 |
| 55 | 105 | 67.7 | 360 | 6 | CQ326482 |
| 56 | 105 | 67.7 | 360 | 6 | AF004432 |
| 57 | 103 | 66.5 | 1408 | 5 | AY485817 |
| 58 | 102 | 65.8 | 732 | 5 | AY485820 |
| 59 | 101 | 65.2 | 892 | 5 | AY485820 |
| 60 | 101 | 65.2 | 1050 | 5 | HSU77612 |
| 61 | 97 | 62.6 | 984 | 5 | AY485816 |
| 62 | 96 | 61.9 | 790 | 5 | AY485816 |
| 63 | 96 | 61.9 | 1300 | 5 | AF324209 |
| 64 | 93 | 60.0 | 796 | 5 | AF159707 |
| 65 | 91 | 58.7 | 738 | 5 | AF159708 |
| 66 | 91 | 58.7 | 974 | 5 | AY485815 |
| 67 | 88 | 56.8 | 1014 | 5 | OMU19914 |
| 68 | 88 | 56.8 | 1041 | 5 | OMU19917 |
| 69 | 88 | 56.8 | 1041 | 5 | S78475 |
| 70 | 85 | 54.8 | 1045 | 5 | AY485809 |
| 71 | 85 | 54.8 | 1045 | 5 | AY485812 |
| 72 | 85 | 54.8 | 2491 | 5 | AY485821 |
| 73 | 84 | 54.2 | 520 | 5 | AY485818 |
| 74 | 83 | 53.5 | 383 | 5 | OMU19913 |
| 75 | 83 | 53.5 | 383 | 5 | OMU19920 |
| 76 | 83 | 53.5 | 400 | 5 | S78473 |
| 77 | 83 | 53.5 | 400 | 5 | S78474 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AY242124 Sus scrofa | AR108106 Sequence | AR108107 Sequence | AR108109 Sequence | A31421 H.sapiens m | CQ729100 Sequence | D00014 Cavia porce | AR270649 Sequence | J04040 Human gluc | M57688 Octodon deg | K00107 Bovine panc | J00059 Syrian hams | AF308439 Cavia fam | BC005278 Homo sapi | AR108119 Sequence | CQ493428 Sequence | CQ414344 Sequence | V01515 Human gene | X03991 Human gluc | AC007750 Homo sapi | AC111919 Rattus no | AC097841 Rattus no | CQ054796 Sequence | CQ074034 Sequence | CQ104933 Sequence | CQ143637 Sequence | CQ179117 Sequence | CQ203473 Sequence | CQ226837 Sequence | CQ264982 Sequence | CQ302070 Sequence | CQ339262 Sequence | Z46845 M.musculus | BC012975 Mus muscu | AF276754 Mus muscu | AL928876 Mouse DNA | AC024141 Mus muscu | AF529185 Ovis arie | AX147453 Sequence | S78477 proglucagon | BC075391 Xenopus t | CQ064797 Sequence | CQ091744 Sequence | CQ130570 Sequence | CQ169179 Sequence | CQ198311 Sequence | CQ213772 Sequence | CQ252355 Sequence | CQ289502 Sequence | CQ326482 Sequence | AF004432 Xenopus l | AY485817 Squallus a | AY485820 Agkistrod | U77612 Heloderma s | AY485816 Neocerato | AY485819 Bufo mari | AF324209 Hoplobatr | AF159707 Petromyzo | AF159708 Petromyzo | AY485815 Protocler | U19914 Oncothychnu | U19917 Oncothychnu | S78475 proglucagon | AY485809 Sebastes | AY485812 Ictalurus | AY485821 Sebastes | AY485818 Hydrolagu | U19913 Oncothychnu | U19920 Oncothychnu | S78473 Oncothychnu | S78474 proglucagon |
|---------------------|-------------------|-------------------|-------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 17, 2005, 16:34:36 ; Search time 2275 Seconds
(without alignments)
619.067 Million cell updates/sec

Title: US-10-042-746-1
Sequence: 1 XHNDGSPSDENMTXLDLAXXDFINMLXKTITDX 37

Scoring table:
BLOSUM62DX
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=xlh
-O/cgm2_1/USPTO.spool/US10042746/runat.17102005.100049.4729/app.query.fasta.1.398
-DB=EST -OPMT=fastap -SUFFIX=est -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-INITs-bits -START=1 -END=1 -MATRIX=bl6sum62DX -TRANS=human40.cdi -LIST=500
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=250 -MODE=LOCAL
-OUTPMT=pct -NORM=ext -HEAPSZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10042746 -CCEN=1.14385 -@runat.17102005.100049.4729 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NMG_SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :
EST :
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 155 | 100.0 | 224 5 | BU951728 ins9h06.y |
| 2 | 155 | 100.0 | 310 5 | BU074812 im7a03.y |
| 3 | 155 | 100.0 | 340 5 | BU785759 ins4h01.y |
| 4 | 155 | 100.0 | 378 5 | BU949819 ins1a03.y |
| 5 | 155 | 100.0 | 384 6 | CB178364 ins7e04.y |
| 6 | 155 | 100.0 | 389 5 | BO632756 ins7e09.y |
| 7 | 155 | 100.0 | 391 6 | CA777022 ip02a11.y |
| 8 | 155 | 100.0 | 400 6 | CB068992 ins3f09.y |
| 9 | 155 | 100.0 | 401 6 | CA949891 iq26h06.y |

| | | | | |
|------|-----|-------|-------|-------------------|
| C 10 | 155 | 100.0 | 403 6 | CA946915 |
| C 11 | 155 | 100.0 | 409 6 | CB070384 |
| C 12 | 155 | 100.0 | 419 6 | EM836042 K-EST011 |
| C 13 | 155 | 100.0 | 420 5 | BQ786903 |
| C 14 | 155 | 100.0 | 421 7 | CK822370 |
| C 15 | 155 | 100.0 | 425 6 | CB178016 |
| C 16 | 155 | 100.0 | 428 5 | BQ271407 |
| C 17 | 155 | 100.0 | 431 5 | BO632226 |
| C 18 | 155 | 100.0 | 434 5 | BM352677 |
| C 19 | 155 | 100.0 | 435 4 | BU74878 |
| C 20 | 155 | 100.0 | 439 5 | BU077375 |
| C 21 | 155 | 100.0 | 441 6 | CA842357 |
| C 22 | 155 | 100.0 | 442 2 | AM190333 |
| C 23 | 155 | 100.0 | 443 6 | CA865479 |
| C 24 | 155 | 100.0 | 446 6 | BQ788028 |
| C 25 | 155 | 100.0 | 450 6 | CA843073 |
| C 26 | 155 | 100.0 | 451 6 | CA948774 |
| C 27 | 155 | 100.0 | 451 4 | BM503895 |
| C 28 | 155 | 100.0 | 451 5 | BQ776591 |
| C 29 | 155 | 100.0 | 451 5 | CB067109 |
| C 30 | 155 | 100.0 | 452 6 | AM243578 |
| C 31 | 155 | 100.0 | 454 5 | BU078231 |
| C 32 | 155 | 100.0 | 454 5 | BU948794 |
| C 33 | 155 | 100.0 | 464 6 | CB178614 |
| C 34 | 155 | 100.0 | 464 6 | CA848770 |
| C 35 | 155 | 100.0 | 466 6 | CB069084 |
| C 36 | 155 | 100.0 | 466 6 | CB069665 |
| C 37 | 155 | 100.0 | 469 6 | BI791800 |
| C 38 | 155 | 100.0 | 470 4 | BM505325 |
| C 39 | 155 | 100.0 | 471 6 | CA948241 |
| C 40 | 155 | 100.0 | 471 6 | BM12561 |
| C 41 | 155 | 100.0 | 473 4 | BI439035 |
| C 42 | 155 | 100.0 | 474 4 | BI467273 |
| C 43 | 155 | 100.0 | 474 4 | CA777299 |
| C 44 | 155 | 100.0 | 475 5 | BM12257 |
| C 45 | 155 | 100.0 | 479 4 | CB067193 |
| C 46 | 155 | 100.0 | 479 6 | CB067193 |
| C 47 | 155 | 100.0 | 482 7 | CB067193 |
| C 48 | 155 | 100.0 | 482 7 | BM312448 |
| C 49 | 155 | 100.0 | 487 5 | BM786347 |
| C 50 | 155 | 100.0 | 488 5 | CA841163 |
| C 51 | 155 | 100.0 | 488 6 | BM509838 |
| C 52 | 155 | 100.0 | 490 4 | BU952083 |
| C 53 | 155 | 100.0 | 492 5 | CA772727 |
| C 54 | 155 | 100.0 | 492 6 | BI791789 |
| C 55 | 155 | 100.0 | 494 4 | BQ271348 |
| C 56 | 155 | 100.0 | 495 5 | BI438781 |
| C 57 | 155 | 100.0 | 496 4 | CB069518 |
| C 58 | 155 | 100.0 | 497 4 | CA948911 |
| C 59 | 155 | 100.0 | 499 6 | CA950017 |
| C 60 | 155 | 100.0 | 499 6 | BI712915 |
| C 61 | 155 | 100.0 | 501 4 | BM504973 |
| C 62 | 155 | 100.0 | 501 6 | BG655424 |
| C 63 | 155 | 100.0 | 504 4 | BG655424 |
| C 64 | 155 | 100.0 | 506 4 | BG655424 |
| C 65 | 155 | 100.0 | 507 5 | BU949129 |
| C 66 | 155 | 100.0 | 508 4 | BG655984 |
| C 67 | 155 | 100.0 | 508 5 | CA776542 |
| C 68 | 155 | 100.0 | 508 6 | CA776542 |
| C 69 | 155 | 100.0 | 509 4 | BI715338 |
| C 70 | 155 | 100.0 | 509 4 | BM315036 |
| C 71 | 155 | 100.0 | 511 5 | BQ632620 |
| C 72 | 155 | 100.0 | 512 6 | CA848560 |
| C 73 | 155 | 100.0 | 513 5 | BU950509 |
| C 74 | 155 | 100.0 | 515 6 | CA867509 |
| C 75 | 155 | 100.0 | 515 6 | CA952216 |
| C 76 | 155 | 100.0 | 516 6 | CA777150 |
| C 77 | 155 | 100.0 | 519 6 | CB067101 |
| C 78 | 155 | 100.0 | 519 6 | BM311172 |
| C 79 | 155 | 100.0 | 521 4 | BG654407 |
| C 80 | 155 | 100.0 | 522 6 | CA842549 |
| C 81 | 155 | 100.0 | 522 6 | CA943101 |
| C 82 | 155 | 100.0 | 522 6 | CA943101 |

| | |
|----------|-------------|
| CA946915 | ins12f03.x |
| CB070384 | ins36e05.y |
| EM836042 | K-EST011 |
| BQ786903 | ins1c09.x |
| CK822370 | ins6a01.x |
| CB178016 | ins24e06.y |
| BQ271407 | ins1k3e06.y |
| BO632226 | ins14b11.x |
| BM352677 | ins69e02.x |
| BU74878 | ins7h03.y |
| BU077375 | ins2e01.y |
| CA842357 | ins24e06.y |
| BU786403 | ins4e01.y |
| AM190333 | ins16a10.x |
| CA865479 | ins14e07.x |
| BQ788028 | ins14e09.x |
| CA843073 | ins3a03.y |
| CA948774 | ins27f01.y |
| BM503895 | ins97b05.y |
| BQ776591 | ins134e04.x |
| CB067109 | ins32b10.y |
| AM243578 | ins3a10.x |
| BU078231 | ins6a12.y |
| BU948794 | ins7h06.x |
| CB178614 | ins37f01.x |
| CA848770 | ins25e05.y |
| CB069084 | ins36e06.y |
| CB069665 | ins26e05.x |
| BI791800 | ins04e03.y |
| BM505325 | ins93d01.x |
| CA948241 | ins199d03.y |
| BM12561 | ins97b07.y |
| BI439035 | ins25e02.y |
| BI467273 | ins22e02.x |
| CA777299 | ins05h04.y |
| BM786347 | ins41h01.y |
| CA841163 | ins94d09.y |
| BM509838 | ins33d04.y |
| BU952083 | ins46e01.y |
| CA772727 | ins46e01.y |
| BI791789 | ins04e11.y |
| BQ271348 | ins12f12.y |
| BI438781 | ins98e01.y |
| CB069518 | ins16e04.y |
| CA948911 | ins29e09.y |
| CA950017 | ins85f08.y |
| BI712915 | ins98h02.y |
| BM504973 | ins33f10.y |
| BG655424 | ins33f10.y |
| BU949129 | ins66e06.x |
| BG655984 | ins35e10.y |
| CA776542 | ins06e03.y |
| CA776542 | ins31e04.y |
| BI715338 | ins31e04.y |
| BM315036 | ins43d08.y |
| BQ632620 | ins125f03.y |
| CA848560 | ins36e02.y |
| BU950509 | ins078e02.y |
| CA867509 | ins29e03.y |
| CA952216 | ins16f09.y |
| CA777150 | ins03e06.y |
| CB067101 | ins32e01.y |
| BM311172 | ins32e01.y |
| BG654407 | ins32e01.y |
| CA842549 | ins32e01.y |
| CA943101 | ins32e01.y |

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OM protein - protein search, using sw model

Run on: October 17, 2005, 15:17:48 ; Search time 54.5 Seconds

(without alignments)
282.986 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XHHADGSPDEMTXLDLXAXDFINLXKTTDX 37

Scoring table: BLOSUM62GX
Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 200 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 155 | 100.0 | 37 | 14 | US-10-042-746-1 |
| 2 | 155 | 100.0 | 37 | 14 | Sequence 1, Appli |
| 3 | 155 | 100.0 | 37 | 15 | US-10-042-746-2 |
| 4 | 155 | 100.0 | 37 | 15 | Sequence 2, Appli |
| 5 | 155 | 100.0 | 37 | 15 | US-10-393-524A-1 |
| 6 | 155 | 100.0 | 37 | 15 | Sequence 4, Appli |
| 7 | 155 | 100.0 | 37 | 15 | US-10-393-524A-4 |
| 8 | 155 | 100.0 | 37 | 15 | Sequence 5, Appli |
| 9 | 155 | 100.0 | 37 | 15 | US-10-393-524A-5 |
| 10 | 155 | 100.0 | 37 | 15 | Sequence 11, Appli |
| 11 | 155 | 100.0 | 37 | 15 | US-10-793-677-1 |
| 12 | 155 | 100.0 | 37 | 15 | Sequence 1, Appli |
| 13 | 155 | 100.0 | 37 | 15 | US-10-793-677-2 |
| 14 | 155 | 100.0 | 37 | 15 | Sequence 198, App |
| 15 | 155 | 100.0 | 37 | 15 | Sequence 199, App |
| 16 | 155 | 100.0 | 37 | 15 | Sequence 200, App |
| 17 | 155 | 100.0 | 37 | 15 | Sequence 201, App |
| 18 | 155 | 100.0 | 37 | 15 | Sequence 202, App |
| 19 | 155 | 100.0 | 37 | 15 | Sequence 203, App |
| 20 | 155 | 100.0 | 37 | 15 | Sequence 204, App |
| 21 | 155 | 100.0 | 37 | 15 | Sequence 205, App |
| 22 | 155 | 100.0 | 37 | 15 | Sequence 206, App |
| 23 | 155 | 100.0 | 37 | 15 | Sequence 207, App |
| 24 | 155 | 100.0 | 37 | 15 | Sequence 208, App |
| 25 | 155 | 100.0 | 37 | 15 | Sequence 209, App |
| 26 | 155 | 100.0 | 37 | 15 | Sequence 210, App |
| 27 | 155 | 100.0 | 37 | 15 | Sequence 211, App |
| 28 | 155 | 100.0 | 37 | 15 | Sequence 212, App |
| 29 | 155 | 100.0 | 37 | 15 | Sequence 213, App |
| 30 | 155 | 100.0 | 37 | 15 | Sequence 214, App |
| 31 | 155 | 100.0 | 37 | 15 | Sequence 215, App |
| 32 | 155 | 100.0 | 37 | 15 | Sequence 216, App |
| 33 | 155 | 100.0 | 37 | 15 | Sequence 217, App |
| 34 | 155 | 100.0 | 37 | 15 | Sequence 218, App |
| 35 | 155 | 100.0 | 37 | 15 | Sequence 219, App |
| 36 | 155 | 100.0 | 37 | 15 | Sequence 220, App |
| 37 | 155 | 100.0 | 37 | 15 | Sequence 221, App |
| 38 | 155 | 100.0 | 37 | 15 | Sequence 222, App |
| 39 | 155 | 100.0 | 37 | 15 | Sequence 223, App |
| 40 | 155 | 100.0 | 37 | 15 | Sequence 224, App |
| 41 | 155 | 100.0 | 37 | 15 | Sequence 225, App |
| 42 | 155 | 100.0 | 37 | 15 | Sequence 226, App |
| 43 | 155 | 100.0 | 37 | 15 | Sequence 227, App |
| 44 | 155 | 100.0 | 37 | 15 | Sequence 228, App |
| 45 | 155 | 100.0 | 37 | 15 | Sequence 229, App |
| 46 | 155 | 100.0 | 37 | 15 | Sequence 230, App |
| 47 | 155 | 100.0 | 37 | 15 | Sequence 231, App |
| 48 | 155 | 100.0 | 37 | 15 | Sequence 232, App |
| 49 | 155 | 100.0 | 37 | 15 | Sequence 233, App |
| 50 | 155 | 100.0 | 37 | 15 | Sequence 234, App |
| 51 | 155 | 100.0 | 37 | 15 | Sequence 235, App |
| 52 | 155 | 100.0 | 37 | 15 | Sequence 236, App |
| 53 | 155 | 100.0 | 37 | 15 | Sequence 237, App |
| 54 | 155 | 100.0 | 37 | 15 | Sequence 238, App |
| 55 | 155 | 100.0 | 37 | 15 | Sequence 239, App |
| 56 | 155 | 100.0 | 37 | 15 | Sequence 240, App |
| 57 | 155 | 100.0 | 37 | 15 | Sequence 241, App |
| 58 | 155 | 100.0 | 37 | 15 | Sequence 242, App |
| 59 | 155 | 100.0 | 37 | 15 | Sequence 243, App |
| 60 | 155 | 100.0 | 37 | 15 | Sequence 244, App |
| 61 | 155 | 100.0 | 37 | 15 | Sequence 245, App |
| 62 | 155 | 100.0 | 37 | 15 | Sequence 246, App |
| 63 | 155 | 100.0 | 37 | 15 | Sequence 247, App |
| 64 | 155 | 100.0 | 37 | 15 | Sequence 248, App |
| 65 | 155 | 100.0 | 37 | 15 | Sequence 249, App |
| 66 | 155 | 100.0 | 37 | 15 | Sequence 250, App |
| 67 | 155 | 100.0 | 37 | 15 | Sequence 251, App |
| 68 | 155 | 100.0 | 37 | 15 | Sequence 252, App |
| 69 | 155 | 100.0 | 37 | 15 | Sequence 253, App |
| 70 | 155 | 100.0 | 37 | 15 | Sequence 254, App |
| 71 | 155 | 100.0 | 37 | 15 | Sequence 255, App |
| 72 | 155 | 100.0 | 37 | 15 | Sequence 256, App |
| 73 | 155 | 100.0 | 37 | 15 | Sequence 257, App |
| 74 | 155 | 100.0 | 37 | 15 | Sequence 258, App |
| 75 | 155 | 100.0 | 37 | 15 | Sequence 259, App |
| 76 | 155 | 100.0 | 37 | 15 | Sequence 260, App |
| 77 | 155 | 100.0 | 37 | 15 | Sequence 261, App |
| 78 | 155 | 100.0 | 37 | 15 | Sequence 262, App |
| 79 | 155 | 100.0 | 37 | 15 | Sequence 263, App |
| 80 | 155 | 100.0 | 37 | 15 | Sequence 264, App |
| 81 | 155 | 100.0 | 37 | 15 | Sequence 265, App |
| 82 | 155 | 100.0 | 37 | 15 | Sequence 266, App |
| 83 | 155 | 100.0 | 37 | 15 | Sequence 267, App |
| 84 | 155 | 100.0 | 37 | 15 | Sequence 268, App |

| | | | | | | |
|----|-----|-------|-----|----|-------------------|-------------------|
| 12 | 155 | 100.0 | 180 | 17 | US-10-775-180-426 | Sequence 426, App |
| 13 | 155 | 100.0 | 180 | 17 | US-10-775-180-427 | Sequence 427, App |
| 14 | 155 | 100.0 | 180 | 17 | US-10-775-180-428 | Sequence 428, App |
| 15 | 155 | 100.0 | 180 | 17 | US-10-775-180-429 | Sequence 429, App |
| 16 | 155 | 100.0 | 180 | 17 | US-10-775-180-430 | Sequence 430, App |
| 17 | 155 | 100.0 | 180 | 17 | US-10-775-180-431 | Sequence 431, App |
| 18 | 155 | 100.0 | 180 | 17 | US-10-775-180-432 | Sequence 432, App |
| 19 | 155 | 100.0 | 180 | 17 | US-10-775-180-433 | Sequence 433, App |
| 20 | 155 | 100.0 | 180 | 17 | US-10-775-180-434 | Sequence 434, App |
| 21 | 155 | 100.0 | 180 | 17 | US-10-775-180-435 | Sequence 435, App |
| 22 | 155 | 100.0 | 180 | 17 | US-10-775-180-436 | Sequence 436, App |
| 23 | 155 | 100.0 | 180 | 17 | US-10-775-180-437 | Sequence 437, App |
| 24 | 155 | 100.0 | 180 | 17 | US-10-775-180-438 | Sequence 438, App |
| 25 | 155 | 100.0 | 180 | 17 | US-10-775-180-439 | Sequence 439, App |
| 26 | 155 | 100.0 | 180 | 17 | US-10-775-180-440 | Sequence 440, App |
| 27 | 155 | 100.0 | 180 | 17 | US-10-775-180-441 | Sequence 441, App |
| 28 | 155 | 100.0 | 180 | 17 | US-10-775-180-442 | Sequence 442, App |
| 29 | 155 | 100.0 | 180 | 17 | US-10-775-180-443 | Sequence 443, App |
| 30 | 155 | 100.0 | 180 | 17 | US-10-775-180-444 | Sequence 444, App |
| 31 | 155 | 100.0 | 180 | 17 | US-10-775-180-445 | Sequence 445, App |
| 32 | 155 | 100.0 | 180 | 17 | US-10-775-180-446 | Sequence 446, App |
| 33 | 155 | 100.0 | 180 | 17 | US-10-775-180-447 | Sequence 447, App |
| 34 | 155 | 100.0 | 180 | 17 | US-10-775-180-448 | Sequence 448, App |
| 35 | 155 | 100.0 | 180 | 17 | US-10-775-180-449 | Sequence 449, App |
| 36 | 155 | 100.0 | 180 | 17 | US-10-775-180-450 | Sequence 450, App |
| 37 | 155 | 100.0 | 180 | 17 | US-10-775-180-451 | Sequence 451, App |
| 38 | 155 | 100.0 | 180 | 17 | US-10-775-180-452 | Sequence 452, App |
| 39 | 155 | 100.0 | 180 | 17 | US-10-775-180-453 | Sequence 453, App |
| 40 | 155 | 100.0 | 180 | 17 | US-10-775-180-454 | Sequence 454, App |
| 41 | 155 | 100.0 | 180 | 17 | US-10-775-180-455 | Sequence 455, App |
| 42 | 155 | 100.0 | 180 | 17 | US-10-775-180-456 | Sequence 456, App |
| 43 | 155 | 100.0 | 180 | 17 | US-10-775-180-457 | Sequence 457, App |
| 44 | 155 | 100.0 | 180 | 17 | US-10-775-180-458 | Sequence 458, App |
| 45 | 155 | 100.0 | 180 | 17 | US-10-775-180-459 | Sequence 459, App |
| 46 | 155 | 100.0 | 180 | 17 | US-10-775-180-460 | Sequence 460, App |
| 47 | 155 | 100.0 | 180 | 17 | US-10-775-180-461 | Sequence 461, App |
| 48 | 155 | 100.0 | 180 | 17 | US-10-775-180-462 | Sequence 462, App |
| 49 | 155 | 100.0 | 180 | 17 | US-10-775-180-463 | Sequence 463, App |
| 50 | 155 | 100.0 | 180 | 17 | US-10-775-180-464 | Sequence 464, App |
| 51 | 155 | 100.0 | 180 | 17 | US-10-775-180-465 | Sequence 465, App |
| 52 | 155 | 100.0 | 180 | 17 | US-10-775-180-466 | Sequence 466, App |
| 53 | 155 | 100.0 | 180 | 17 | US-10-775-180-467 | Sequence 467, App |
| 54 | 155 | 100.0 | 180 | 17 | US-10-775-180-468 | Sequence 468, App |
| 55 | 155 | 100.0 | 180 | 17 | US-10-775-180-469 | Sequence 469, App |
| 56 | 155 | 100.0 | 180 | 17 | US-10-775-180-470 | Sequence 470, App |
| 57 | 155 | 100.0 | 180 | 17 | US-10-775-180-471 | Sequence 471, App |
| 58 | 155 | 100.0 | 180 | 17 | US-10-775-180-472 | Sequence 472, App |
| 59 | 155 | 100.0 | 180 | 17 | US-10-775-180-473 | Sequence 473, App |
| 60 | 155 | 100.0 | 180 | 17 | US-10-775-180-474 | Sequence 474, App |
| 61 | 155 | 100.0 | 180 | 17 | US-10-775-180-475 | Sequence 475, App |
| 62 | 155 | 100.0 | 180 | 17 | US-10-775-180-476 | Sequence 476, App |
| 63 | 155 | 100.0 | 180 | 17 | US-10-775-180-477 | Sequence 477, App |
| 64 | 155 | 100.0 | 180 | 17 | US-10-775-180-478 | Sequence 478, App |
| 65 | 155 | 100.0 | 180 | 17 | US-10-775-180-479 | Sequence 479, App |
| 66 | 155 | 100.0 | 180 | 17 | US-10-775-180-480 | Sequence 480, App |
| 67 | 155 | 100.0 | 180 | 17 | US-10-775-180-481 | Sequence 481, App |
| 68 | 155 | 100.0 | 180 | 17 | US-10-775-180-482 | Sequence 482, App |
| 69 | 155 | 100.0 | 180 | 17 | US-10-775-180-483 | Sequence 483, App |
| 70 | 155 | 100.0 | 180 | 17 | US-10-775-180-484 | Sequence 484, App |
| 71 | 155 | 100.0 | 180 | 17 | US-10-775-180-485 | Sequence 485, App |
| 72 | 155 | 100.0 | 180 | 17 | US-10-775-180-486 | Sequence 486, App |
| 73 | 155 | 100.0 | 180 | 17 | US-10-775-180-487 | Sequence 487, App |
| 74 | 155 | 100.0 | 180 | 17 | US-10-775-180-488 | Sequence 488, App |
| 75 | 155 | 100.0 | 180 | 17 | US-10-775-180-489 | Sequence 489, App |
| 76 | 155 | 100.0 | 180 | 17 | US-10-775-180-490 | Sequence 490, App |
| 77 | 155 | 100.0 | 180 | 17 | US-10-775-180-491 | Sequence 491, App |
| 78 | 155 | 100.0 | 180 | 17 | US-10-775-180-492 | Sequence 492, App |
| 79 | 155 | 100.0 | 180 | 17 | US-10-775-180-493 | Sequence 493, App |
| 80 | 155 | 100.0 | 180 | 17 | US-10-775-180-494 | Sequence 494, App |
| 81 | 155 | 100.0 | 180 | 17 | US-10-775-180-495 | Sequence 495, App |
| 82 | 155 | 100.0 | 180 | 17 | US-10-775-180-496 | Sequence 496, App |
| 83 | 155 | 100.0 | 180 | 17 | US-10-775-180-497 | Sequence 497, App |
| 84 | 155 | 100.0 | 180 | 17 | US-10-775-180-498 | Sequence 498, App |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 14:54:46 ; Search time 52.5 Seconds

(without alignments)
52.610 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155
Sequence: 1 XKHADGSPDEMTXLDLXAXDFIWMXXITTDXX 37Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6C_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | * Query Match | Length | DB ID | Description |
|------------|-------|------------------|--------|-------|------------------|
| 1 | 155 | 100.0 | 37 | 2 | US-08-669-790C-1 |
| 2 | 155 | 100.0 | 37 | 2 | US-08-669-790C-2 |
| 3 | 155 | 100.0 | 37 | 2 | US-08-422-540A-1 |
| 4 | 155 | 100.0 | 37 | 2 | US-08-422-540A-2 |
| 5 | 155 | 100.0 | 37 | 2 | US-08-422-540A-4 |
| 6 | 155 | 100.0 | 37 | 2 | US-08-422-540A-5 |
| 7 | 155 | 100.0 | 37 | 2 | US-08-422-540A-6 |
| 8 | 155 | 100.0 | 37 | 2 | US-08-422-540A-7 |
| 9 | 155 | 100.0 | 180 | 3 | US-08-784-582-56 |
| 10 | 155 | 100.0 | 180 | 3 | US-08-784-582-58 |
| 11 | 155 | 100.0 | 180 | 3 | US-08-784-582-61 |
| 12 | 155 | 100.0 | 360 | 3 | US-08-784-582-73 |
| 13 | 153 | 98.7 | 48 | 2 | US-08-808-825-8 |
| 14 | 151 | 97.4 | 33 | 1 | US-08-669-791C-2 |
| 15 | 151 | 97.4 | 33 | 2 | US-08-669-790C-3 |
| 16 | 151 | 97.4 | 33 | 2 | US-08-669-790C-4 |
| 17 | 151 | 97.4 | 33 | 2 | US-08-808-825-5 |
| 18 | 151 | 97.4 | 33 | 2 | US-08-808-825-6 |
| 19 | 151 | 97.4 | 33 | 2 | US-08-808-825-7 |
| 20 | 151 | 97.4 | 33 | 2 | US-08-422-540A-3 |
| 21 | 151 | 97.4 | 33 | 3 | US-08-835-538C-2 |
| 22 | 151 | 97.4 | 33 | 3 | US-09-149-831-1 |
| 23 | 151 | 97.4 | 33 | 3 | US-09-149-831-2 |
| 24 | 151 | 97.4 | 33 | 4 | US-09-233-934-1 |
| 25 | 151 | 97.4 | 33 | 4 | US-09-692-238-1 |
| 26 | 151 | 97.4 | 33 | 4 | US-09-692-238-2 |
| 27 | 147 | 94.8 | 33 | 1 | US-08-669-791C-5 |

| | | | | | | |
|-----|-----|------|-----|---|--------------------|-------------------|
| 28 | 140 | 90.3 | 35 | 2 | US-08-808-825-1 | Sequence 1, Appl |
| 29 | 79 | 51.0 | 31 | 1 | US-08-062-472B-42 | Sequence 42, Appl |
| 30 | 79 | 51.0 | 69 | 1 | US-08-193-863-1 | Sequence 1, Appl |
| 31 | 79 | 51.0 | 69 | 1 | US-08-377-833-1 | Sequence 1, Appl |
| 32 | 79 | 51.0 | 69 | 1 | US-08-324-502-1 | Sequence 1, Appl |
| 33 | 79 | 51.0 | 69 | 1 | US-08-083-501-1 | Sequence 1, Appl |
| 34 | 79 | 51.0 | 69 | 1 | US-08-415-939-1 | Sequence 1, Appl |
| 35 | 79 | 51.0 | 69 | 1 | US-08-548-152-1 | Sequence 1, Appl |
| 36 | 79 | 51.0 | 70 | 1 | US-08-193-863-2 | Sequence 2, Appl |
| 37 | 79 | 51.0 | 70 | 1 | US-08-377-833-2 | Sequence 2, Appl |
| 38 | 79 | 51.0 | 70 | 1 | US-08-324-502-2 | Sequence 2, Appl |
| 39 | 79 | 51.0 | 70 | 1 | US-08-083-501-2 | Sequence 2, Appl |
| 40 | 79 | 51.0 | 70 | 1 | US-08-415-939-2 | Sequence 2, Appl |
| 41 | 77 | 49.7 | 38 | 3 | US-09-258-750-84 | Sequence 84, Appl |
| 42 | 77 | 49.7 | 38 | 4 | US-09-398-111-84 | Sequence 84, Appl |
| 43 | 77 | 49.7 | 39 | 3 | US-09-258-750-91 | Sequence 91, Appl |
| 44 | 77 | 49.7 | 39 | 4 | US-09-398-111-91 | Sequence 91, Appl |
| 45 | 76 | 49.0 | 29 | 4 | US-09-847-249A-43 | Sequence 43, Appl |
| 46 | 76 | 49.0 | 30 | 4 | US-09-268-578C-14 | Sequence 14, Appl |
| 47 | 76 | 49.0 | 30 | 4 | US-09-268-578C-49 | Sequence 49, Appl |
| 48 | 76 | 49.0 | 30 | 4 | US-09-268-578C-55 | Sequence 55, Appl |
| 49 | 76 | 49.0 | 156 | 4 | US-09-949-016-9452 | Sequence 9452, Ap |
| 50 | 75 | 48.4 | 29 | 4 | US-09-847-249A-9 | Sequence 9, Appl |
| 51 | 75 | 48.4 | 29 | 4 | US-09-847-249A-10 | Sequence 10, Appl |
| 52 | 75 | 48.4 | 29 | 4 | US-09-847-249A-11 | Sequence 11, Appl |
| 53 | 75 | 48.4 | 29 | 4 | US-09-847-249A-44 | Sequence 44, Appl |
| 54 | 75 | 48.4 | 29 | 4 | US-09-847-249A-51 | Sequence 51, Appl |
| 55 | 75 | 48.4 | 29 | 4 | US-09-847-249A-59 | Sequence 59, Appl |
| 56 | 75 | 48.4 | 30 | 4 | US-09-147-345A-36 | Sequence 36, Appl |
| 57 | 75 | 48.4 | 31 | 3 | US-09-258-750-3 | Sequence 3, Appl |
| 58 | 75 | 48.4 | 31 | 3 | US-09-258-750-4 | Sequence 4, Appl |
| 59 | 75 | 48.4 | 31 | 3 | US-09-258-750-8 | Sequence 8, Appl |
| 60 | 75 | 48.4 | 31 | 3 | US-09-258-750-9 | Sequence 9, Appl |
| 61 | 75 | 48.4 | 31 | 4 | US-09-398-111-3 | Sequence 3, Appl |
| 62 | 75 | 48.4 | 31 | 4 | US-09-398-111-4 | Sequence 4, Appl |
| 63 | 75 | 48.4 | 31 | 4 | US-09-398-111-8 | Sequence 8, Appl |
| 64 | 75 | 48.4 | 31 | 4 | US-09-398-111-9 | Sequence 9, Appl |
| 65 | 75 | 48.4 | 32 | 3 | US-09-258-750-5 | Sequence 5, Appl |
| 66 | 75 | 48.4 | 32 | 3 | US-09-258-750-87 | Sequence 87, Appl |
| 67 | 75 | 48.4 | 32 | 4 | US-09-398-111-5 | Sequence 5, Appl |
| 68 | 75 | 48.4 | 32 | 4 | US-09-398-111-87 | Sequence 87, Appl |
| 69 | 75 | 48.4 | 33 | 3 | US-09-258-750-12 | Sequence 12, Appl |
| 70 | 75 | 48.4 | 33 | 3 | US-09-258-750-94 | Sequence 94, Appl |
| 71 | 75 | 48.4 | 33 | 4 | US-09-398-111-12 | Sequence 12, Appl |
| 72 | 75 | 48.4 | 33 | 4 | US-09-398-111-94 | Sequence 94, Appl |
| 73 | 75 | 48.4 | 34 | 3 | US-09-258-750-13 | Sequence 13, Appl |
| 74 | 75 | 48.4 | 34 | 3 | US-09-398-111-13 | Sequence 13, Appl |
| 75 | 75 | 48.4 | 42 | 3 | US-09-268-846-21 | Sequence 21, Appl |
| 76 | 75 | 48.4 | 187 | 2 | US-08-835-221-16 | Sequence 16, Appl |
| 77 | 75 | 48.4 | 187 | 2 | US-09-108-661-16 | Sequence 16, Appl |
| 78 | 74 | 47.7 | 29 | 4 | US-09-847-249A-72 | Sequence 72, Appl |
| 79 | 74 | 47.7 | 34 | 1 | US-08-095-162-6 | Sequence 6, Appl |
| 80 | 74 | 47.7 | 34 | 1 | US-08-470-220A-6 | Sequence 6, Appl |
| 81 | 74 | 47.7 | 34 | 3 | US-08-967-374-6 | Sequence 6, Appl |
| 82 | 74 | 47.7 | 34 | 3 | US-08-258-750-66 | Sequence 66, Appl |
| 83 | 74 | 47.7 | 34 | 4 | US-09-505-991-6 | Sequence 6, Appl |
| 84 | 74 | 47.7 | 34 | 4 | US-09-398-111-66 | Sequence 66, Appl |
| 85 | 74 | 47.7 | 34 | 4 | US-09-212-663-25 | Sequence 25, Appl |
| 86 | 74 | 47.7 | 34 | 5 | PCT-US95-15800-26 | Sequence 26, Appl |
| 87 | 74 | 47.7 | 35 | 3 | US-09-258-750-58 | Sequence 58, Appl |
| 88 | 74 | 47.7 | 35 | 3 | US-09-258-750-67 | Sequence 67, Appl |
| 89 | 74 | 47.7 | 35 | 4 | US-09-398-111-58 | Sequence 58, Appl |
| 90 | 74 | 47.7 | 35 | 4 | US-09-398-111-67 | Sequence 67, Appl |
| 91 | 74 | 47.7 | 36 | 1 | US-08-095-162-15 | Sequence 15, Appl |
| 92 | 74 | 47.7 | 36 | 1 | US-08-470-220A-15 | Sequence 15, Appl |
| 93 | 74 | 47.7 | 36 | 2 | US-08-808-825-9 | Sequence 9, Appl |
| 94 | 74 | 47.7 | 36 | 2 | US-08-899-324-1 | Sequence 1, Appl |
| 95 | 74 | 47.7 | 36 | 3 | US-08-967-374-15 | Sequence 15, Appl |
| 96 | 74 | 47.7 | 36 | 3 | US-08-339-892B-1 | Sequence 1, Appl |
| 97 | 74 | 47.7 | 36 | 3 | US-09-258-750-59 | Sequence 59, Appl |
| 98 | 74 | 47.7 | 36 | 3 | US-09-258-750-68 | Sequence 68, Appl |
| 99 | 74 | 47.7 | 36 | 3 | US-09-302-596-2 | Sequence 2, Appl |
| 100 | 74 | 47.7 | 36 | 3 | | |

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OM protein - protein search, using sw model

Run on: October 17, 2005, 12:43:07 ; Search time 56 Seconds
(without alignments)
255,538 Million cell updates/sec

Title: US-10-042-746-1

Sequence: 1 XKHADGSFSDENMTXLDXLAAXDFINWXXITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : A_Geneseq15Dec04:*

- 1: geneseqp1808:*
- 2: geneseqp1808:*
- 3: geneseqp20006:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 155 | 100.0 | 37 | 5 | ABR79376 Glucagon- |
| 2 | 155 | 100.0 | 37 | 7 | ADP43243 Rat/human |
| 3 | 155 | 100.0 | 37 | 7 | ADP43244 Rat/human |
| 4 | 155 | 100.0 | 180 | 2 | AAW16384 Rat prepr |
| 5 | 155 | 100.0 | 180 | 2 | AAW22081 Human pre |
| 6 | 155 | 100.0 | 180 | 2 | AAW22079 Rat prepr |
| 7 | 155 | 100.0 | 180 | 2 | AAW22080 Human pre |
| 8 | 155 | 100.0 | 180 | 3 | AAW39812 Preproglu |
| 9 | 155 | 100.0 | 180 | 3 | AAW36773 Rat prepr |
| 10 | 155 | 100.0 | 180 | 3 | AAW66774 Human pre |
| 11 | 155 | 100.0 | 180 | 3 | AAW66775 Mutant hu |
| 12 | 155 | 100.0 | 180 | 7 | ADP15331 Human alb |
| 13 | 155 | 100.0 | 180 | 7 | ADP16673 Human alb |
| 14 | 155 | 100.0 | 180 | 7 | ADP15333 Human alb |
| 15 | 155 | 100.0 | 180 | 7 | ADP15335 Human alb |
| 16 | 155 | 100.0 | 180 | 7 | ADP16161 Human alb |
| 17 | 155 | 100.0 | 180 | 7 | ADP16162 Human alb |
| 18 | 155 | 100.0 | 180 | 7 | ADP16160 Human alb |
| 19 | 155 | 100.0 | 180 | 7 | ADP16674 Human alb |
| 20 | 155 | 100.0 | 180 | 7 | ADP16163 Human alb |
| 21 | 155 | 100.0 | 180 | 7 | ADP15333 Human alb |
| 22 | 155 | 100.0 | 180 | 7 | ADP16625 Human alb |
| 23 | 155 | 100.0 | 180 | 7 | ADP16159 Human alb |
| 24 | 155 | 100.0 | 180 | 7 | ADH21631 Human GLP |
| 25 | 155 | 100.0 | 180 | 7 | ADH21878 Human GLP |

| | | | | | |
|----|-----|-------|-----|---|---------------------|
| 26 | 155 | 100.0 | 180 | 7 | ADH21633 Human GLP |
| 27 | 155 | 100.0 | 180 | 7 | ADH21403 Human GLP |
| 28 | 155 | 100.0 | 180 | 7 | ADH21630 Human GLP |
| 29 | 155 | 100.0 | 180 | 7 | ADH21401 Human GLP |
| 30 | 155 | 100.0 | 180 | 7 | ADH21404 Human GLP |
| 31 | 155 | 100.0 | 180 | 7 | ADH21402 Human GLP |
| 32 | 155 | 100.0 | 180 | 7 | ADH21632 Human GLP |
| 33 | 155 | 100.0 | 180 | 7 | ADH21854 Human GLP |
| 34 | 155 | 100.0 | 180 | 7 | ADH21629 Human GLP |
| 35 | 155 | 100.0 | 180 | 7 | ADH21879 Human GLP |
| 36 | 155 | 100.0 | 180 | 8 | ADH88908 Human pre |
| 37 | 155 | 100.0 | 360 | 3 | AAW66777 Human gro |
| 38 | 153 | 98.7 | 35 | 2 | AAW93735 Glucagon- |
| 39 | 153 | 98.7 | 35 | 2 | AAW66204 Arg35-GLP |
| 40 | 153 | 98.7 | 35 | 2 | AAW66210 Arg35, Lys |
| 41 | 153 | 98.7 | 35 | 8 | ADL56789 Rat gluc |
| 42 | 153 | 98.7 | 35 | 8 | ADL56787 Rat gluc |
| 43 | 153 | 98.7 | 35 | 8 | ADL56788 Rat gluc |
| 44 | 153 | 98.7 | 47 | 4 | AAW14137 Peptide # |
| 45 | 153 | 98.7 | 47 | 4 | AAW33082 Peptide # |
| 46 | 153 | 98.7 | 47 | 4 | AAW26543 Peptide # |
| 47 | 153 | 98.7 | 47 | 4 | ABW27910 Human pep |
| 48 | 153 | 98.7 | 47 | 4 | ABW18550 Protein # |
| 49 | 153 | 98.7 | 47 | 4 | AAW66267 Human bon |
| 50 | 153 | 98.7 | 47 | 4 | AAW53879 Human bra |
| 51 | 153 | 98.7 | 47 | 4 | ABW47931 Human liv |
| 52 | 153 | 98.7 | 47 | 4 | AAW01875 Peptide # |
| 53 | 153 | 98.7 | 47 | 5 | ABW35914 Human pep |
| 54 | 153 | 98.7 | 48 | 2 | AAW35944 N-termina |
| 55 | 152 | 98.1 | 34 | 2 | AAW93733 Glucagon- |
| 56 | 152 | 98.1 | 34 | 2 | AAW04341 Glucagon- |
| 57 | 152 | 98.1 | 34 | 2 | AAW93734 Glucagon- |
| 58 | 152 | 98.1 | 34 | 2 | AAW45330 Glucagon- |
| 59 | 152 | 98.1 | 34 | 2 | AAW45333 Glucagon- |
| 60 | 152 | 98.1 | 34 | 2 | AAW66203 GLP-2 (1- |
| 61 | 152 | 98.1 | 34 | 4 | AAW91172 Pancreat |
| 62 | 152 | 98.1 | 34 | 4 | ABW56999 Human glu |
| 63 | 152 | 98.1 | 34 | 4 | ABW57003 Human glu |
| 64 | 152 | 98.1 | 34 | 5 | AAW022954 Glucagon- |
| 65 | 152 | 98.1 | 34 | 5 | AAW022963 Glucagon- |
| 66 | 152 | 98.1 | 34 | 5 | AAW022972 Glucagon- |
| 67 | 152 | 98.1 | 34 | 5 | AAW026002 Glucagon- |
| 68 | 152 | 98.1 | 34 | 5 | AAW022944 Glucagon- |
| 69 | 152 | 98.1 | 34 | 8 | ADP90105 GLP-2 (1-3 |
| 70 | 152 | 98.1 | 34 | 8 | ADG74830 GLP-2 pre |
| 71 | 151 | 97.4 | 33 | 2 | AAW04342 Glucagon- |
| 72 | 151 | 97.4 | 33 | 2 | AAW04343 Glucagon- |
| 73 | 151 | 97.4 | 33 | 2 | AAW45262 Glucagon- |
| 74 | 151 | 97.4 | 33 | 2 | AAW45290 Glucagon- |
| 75 | 151 | 97.4 | 33 | 2 | AAW45319 Glucagon- |
| 76 | 151 | 97.4 | 33 | 2 | AAW45328 Glucagon- |
| 77 | 151 | 97.4 | 33 | 2 | AAW45324 Glucagon- |
| 78 | 151 | 97.4 | 33 | 2 | AAW45324 Glucagon- |
| 79 | 151 | 97.4 | 33 | 2 | AAW35941 Human GLP |
| 80 | 151 | 97.4 | 33 | 2 | AAW35942 Rat GLP-2 |
| 81 | 151 | 97.4 | 33 | 2 | AAW35943 Porcine G |
| 82 | 151 | 97.4 | 33 | 2 | AAW66205 Lys20(N-e |
| 83 | 151 | 97.4 | 33 | 2 | AAW66205 Lys20 (1- |
| 84 | 151 | 97.4 | 33 | 2 | AAW66206 Lys20, 30- |
| 85 | 151 | 97.4 | 33 | 2 | AAW61439 Human GLP |
| 86 | 151 | 97.4 | 33 | 2 | AAW45784 Human glu |
| 87 | 151 | 97.4 | 33 | 2 | AAW94485 Rat gluc |
| 88 | 151 | 97.4 | 33 | 2 | AAW94484 Human glu |
| 89 | 151 | 97.4 | 33 | 2 | AAW01241 Human glu |
| 90 | 151 | 97.4 | 33 | 2 | AAW01240 Rat gluc |
| 91 | 151 | 97.4 | 33 | 2 | AAW01242 Rat gluc |
| 92 | 151 | 97.4 | 33 | 4 | AAW62009 Human wil |
| 93 | 151 | 97.4 | 33 | 4 | AAW91171 Pancreat |
| 94 | 151 | 97.4 | 33 | 4 | AAW65842 Rat gluc |
| 95 | 151 | 97.4 | 33 | 4 | AAW65841 Human glu |
| 96 | 151 | 97.4 | 33 | 4 | AAW65935 Human glu |
| 97 | 151 | 97.4 | 33 | 4 | ABW56867 Human glu |
| 98 | 151 | 97.4 | 33 | 4 | ABW56905 Rat gluc |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:03:46 ; Search time 199.5 Seconds

(without alignments)
94.972 Million cell updates/sec

Title: US-10-042-746-1

Perfect score: 155

Sequence: 1 XXHADSGSFSDENMTXLDLXAXDFINWLXXTKITDX 37

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 155 | 100.0 | 80 2 | Q61U88 phodopus su |
| 2 | 155 | 100.0 | 180 1 | GLUC_BOVIN |
| 3 | 155 | 100.0 | 180 1 | GLUC_CANFA |
| 4 | 155 | 100.0 | 180 1 | GLUC_CAVPO |
| 5 | 155 | 100.0 | 180 1 | GLUC_HUMAN |
| 6 | 155 | 100.0 | 180 1 | GLUC_MESAU |
| 7 | 155 | 100.0 | 180 1 | GLUC_OCTDE |
| 8 | 155 | 100.0 | 180 1 | GLUC_PIG |
| 9 | 155 | 100.0 | 180 1 | GLUC_RAT |
| 10 | 150 | 96.8 | 180 1 | GLUC_MOUSE |
| 11 | 142 | 91.6 | 176 1 | GLUC_SHEEP |
| 12 | 109 | 70.3 | 206 1 | GLUC_CHICK |
| 13 | 109 | 70.3 | 266 2 | Q6D1Z4 |
| 14 | 103 | 66.5 | 266 1 | GLUC_XENLA |
| 15 | 102 | 65.8 | 170 2 | Q6RYB4 |
| 16 | 101 | 65.2 | 124 2 | Q6RYB1 |
| 17 | 101 | 65.2 | 124 2 | GLUC_HELSU |
| 18 | 97 | 62.6 | 145 2 | Q6RYB5 |
| 19 | 96 | 61.9 | 149 2 | Q6RYB2 |
| 20 | 96 | 61.9 | 220 2 | Q6UWL9 |
| 21 | 94 | 60.6 | 103 1 | GLUC_RANCA |
| 22 | 93 | 60.0 | 160 1 | GLUC_PETMA |
| 23 | 91 | 58.7 | 120 1 | GLUC_PETMA |
| 24 | 91 | 58.7 | 153 2 | Q6RYB6 |
| 25 | 88 | 56.8 | 178 1 | GLUC_ONCMY |
| 26 | 88 | 56.8 | 178 1 | GLUC_ONCMY |
| 27 | 85 | 54.8 | 173 2 | Q6RYB3 |
| 28 | 85 | 54.8 | 176 2 | Q6RYB2 |
| 29 | 85 | 54.8 | 176 2 | Q6RYB3 |
| 30 | 84 | 54.2 | 173 2 | Q6RYB3 |
| 31 | 83 | 53.5 | 66 2 | Q788W6 |

| | | | | | |
|-----|------|------|--------|------------|-----------------------|
| 32 | 83 | 53.5 | 72 2 | Q91409 | Q91409 oncorhynch |
| 33 | 83 | 53.5 | 122 2 | Q6RYB8 | Q6RYB8 ictalurus p |
| 34 | 82 | 52.9 | 36 1 | GLUC_HYDCC | P09682 hydroclaus |
| 35 | 81 | 52.3 | 68 1 | GLUC_ONCKI | P07449 oncorhynch |
| 36 | 79 | 51.0 | 71 1 | GLUC_ICTPU | P04093 ictalurus p |
| 37 | 79 | 51.0 | 122 1 | GLUC_LOBAM | P04092 lophus ame |
| 38 | 79 | 51.0 | 219 1 | GLUC_XENLA | Q42144 xenopus lae |
| 39 | 78 | 50.3 | 71 1 | GLUC_PIRME | P41880 piractus m |
| 40 | 78 | 50.3 | 78 1 | GLUC_LBSP | P09566 lepisosteus |
| 41 | 78 | 50.3 | 120 2 | Q6RYB7 | Q6RYB7 ictalurus p |
| 42 | 77 | 49.7 | 49 1 | GLUC_CALMI | P31189 callorhynch |
| 43 | 77 | 49.7 | 62 1 | GLUC_SCYA | P09687 scyllorhynch |
| 44 | 77 | 49.7 | 121 1 | GLUC_CAVAU | P79695 carassius a |
| 45 | 77 | 49.7 | 123 2 | Q6RYA9 | Q6RYA9 sebastes ca |
| 46 | 77 | 49.7 | 144 2 | GIP_RAT | GIP_RAT rattus norv |
| 47 | 76 | 49.0 | 30 2 | Q6RYN3 | Q6RYN3 polyodon sp |
| 48 | 76 | 49.0 | 121 2 | Q6RYC1 | Q6RYC1 sebastes ca |
| 49 | 76 | 49.0 | 121 2 | Q9DD66 | Q9DD66 brachydanio |
| 50 | 76 | 49.0 | 153 1 | GIP_HUMAN | GIP_HUMAN homo sapien |
| 51 | 76 | 49.0 | 153 2 | Q6NTD3 | Q6NTD3 homo sapien |
| 52 | 75 | 48.4 | 42 1 | GIP_BOVIN | GIP_BOVIN bos taurus |
| 53 | 75 | 48.4 | 42 1 | GIP_PIG | P01281 sus scrofa |
| 54 | 74 | 47.7 | 29 1 | GLUC_TORMA | P09567 torpedo mar |
| 55 | 74 | 47.7 | 36 1 | GLUC_ORENI | P81026 oreochromis |
| 56 | 74 | 47.7 | 45 2 | Q6PRF4 | Q6PRF4 capra hircu |
| 57 | 74 | 47.7 | 130 2 | Q9CVF1 | Q9CVF1 mus musculu |
| 58 | 74 | 47.7 | 144 2 | GIP_MOUSE | P48756 mus musculu |
| 59 | 74 | 47.7 | 144 2 | Q9DB87 | Q9DB87 mus musculu |
| 60 | 72 | 46.5 | 29 1 | GLUC_ANAPL | P01276 anas platyr |
| 61 | 72 | 46.5 | 29 1 | GLUC_CAMPD | P68273 canelis dro |
| 62 | 72 | 46.5 | 29 1 | GLUC_DIDMA | P18108 didelphis m |
| 63 | 72 | 46.5 | 29 1 | GLUC_LAMFL | Q39393 lampetra fl |
| 64 | 72 | 46.5 | 29 1 | GLUC_MELGA | P68260 melagreta g |
| 65 | 72 | 46.5 | 29 1 | GLUC_RABIT | P68274 oryctolagus |
| 66 | 72 | 46.5 | 29 1 | GLUC_SAISS | P68275 saimiri sci |
| 67 | 72 | 46.5 | 96 1 | GLUC_MYOSC | P09666 myoxocephal |
| 68 | 72 | 46.5 | 124 1 | GLUC_LOBAM | P01278 lophus ame |
| 69 | 72 | 46.5 | 500 2 | Q849W5 | Q849W5 escherichia |
| 70 | 71 | 45.8 | 75 1 | GLUC_AMICA | P33528 amia calva |
| 71 | 70 | 45.2 | 29 1 | GLUC_PLAFB | P23062 platichthys |
| 72 | 70 | 45.2 | 96 2 | Q9DG43 | Q9DG43 anguilla an |
| 73 | 69 | 44.5 | 30 1 | GLUC_ANGRO | P63295 anguilla ro |
| 74 | 69 | 44.5 | 29 1 | GLUC_CHIBR | P31297 chinchilla |
| 75 | 67 | 43.2 | 87 2 | Q7SZU6 | Q7SZU6 heloderma h |
| 76 | 67 | 43.2 | 39 1 | EXE3_HELHO | Q23034 heloderma h |
| 77 | 65 | 41.9 | 679 2 | Q23352 | Q23352 arabisidopsis |
| 78 | 65 | 41.9 | 787 2 | Q94C98 | Q94C98 arabidopsis |
| 79 | 65 | 41.9 | 31 2 | Q7LZN2 | Q7LZN2 polyodon sp |
| 80 | 63 | 40.6 | 928 1 | MAY4_SCHCO | P37935 schizophylli |
| 81 | 62.5 | 40.3 | 87 1 | EXE4_HELSU | P26349 heloderma s |
| 82 | 62 | 40.0 | 387 2 | Q8FSR2 | Q8FSR2 corynebacte |
| 83 | 62 | 40.0 | 754 2 | Q8LZG6 | Q8LZG6 mus musculu |
| 84 | 62 | 40.0 | 2152 2 | Q09515 | Q09515 caenorhabdi |
| 85 | 62 | 40.0 | 145 2 | Q7N1M1 | Q7N1M1 photorhabdu |
| 86 | 61.5 | 39.7 | 31 2 | Q7LZN4 | Q7LZN4 polyodon sp |
| 87 | 61 | 39.4 | 502 2 | Q9R841 | Q9R841 deinococcus |
| 88 | 61 | 39.4 | 712 2 | Q92R80 | Q92R80 rhabdium m |
| 89 | 61 | 39.4 | 1072 2 | HSER_RAT | P23897 rattus norv |
| 90 | 61 | 39.4 | 344 2 | Q12347 | Q12347 saccharomyc |
| 91 | 60 | 38.7 | 572 2 | Q882W2 | Q882W2 pseudomonas |
| 92 | 60 | 38.7 | 639 2 | Q9C8S3 | Q9C8S3 lactococcus |
| 93 | 60 | 38.7 | 544 2 | Q8RCL9 | Q8RCL9 thermomanaer |
| 94 | 59.5 | 38.4 | 94 2 | Q76ZG6 | Q76ZG6 bacteriophag |
| 95 | 59 | 38.1 | 145 2 | Q7MXY9 | Q7MXY9 macaca fasc |
| 96 | 59 | 38.1 | 170 1 | VIP_BOVIN | P81801 bos taurus |
| 97 | 59 | 38.1 | 170 1 | VIP_HUMAN | P01282 homo sapien |
| 98 | 59 | 38.1 | 205 2 | Q9T7Z5 | Q9T7Z5 oryctolagus |
| 99 | 59 | 38.1 | 295 2 | Q62832 | Q62832 bos taurus |
| 100 | 59 | 38.1 | 518 2 | Q38233 | Q38233 lactococcus |
| 101 | 59 | 38.1 | 518 2 | Q38307 | Q38307 lactococcus |
| 102 | 59 | 38.1 | 1076 1 | HSER_CAVPO | P70106 cavia porce |
| 103 | 59 | 38.1 | 1967 2 | Q7RHF3 | Q7RHF3 plasmodium |
| 104 | 59 | 38.1 | | | |

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OM protein - protein search, using sw model

Run on: October 16, 2005, 10:55:31 ; Search time 38.5 Seconds

(without alignments)
92.468 Million cell updates/sec

Title: US-10-042-746-1

Perfile score: 155
Sequence: 1 XXHADGFSFSDENMTXLDLAXXDFFINMLXXRTITDX 37

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 155 | 100.0 | 180 | 1 | GCXY glucagon precursor |
| 2 | 155 | 100.0 | 180 | 1 | GCYP glucagon precursor |
| 3 | 155 | 100.0 | 180 | 1 | GCYU glucagon precursor |
| 4 | 155 | 100.0 | 180 | 1 | GCRT glucagon precursor |
| 5 | 155 | 100.0 | 180 | 1 | GCRTDU glucagon precursor |
| 6 | 153 | 98.7 | 158 | 1 | GCPR glucagon precursor |
| 7 | 150 | 96.8 | 180 | 2 | A57294 glucagon precursor |
| 8 | 148 | 95.5 | 180 | 1 | GCBO glucagon precursor |
| 9 | 109 | 70.3 | 206 | 2 | 151301 glucagon precursor |
| 10 | 94 | 60.6 | 101 | 1 | IS057 glucagon precursor |
| 11 | 88 | 56.8 | 178 | 2 | 151058 glucagon precursor |
| 12 | 88 | 56.8 | 178 | 2 | 151058 glucagon precursor |
| 13 | 83 | 53.5 | 66 | 2 | 151093 glucagon precursor |
| 14 | 82 | 52.9 | 36 | 1 | GCRT glucagon precursor |
| 15 | 81 | 52.3 | 60 | 1 | GCRT glucagon precursor |
| 16 | 79 | 51.0 | 63 | 1 | GCRT glucagon precursor |
| 17 | 79 | 51.0 | 69 | 1 | GCRT glucagon precursor |
| 18 | 79 | 51.0 | 122 | 1 | GCRT glucagon precursor |
| 19 | 78 | 51.0 | 151 | 1 | GCRT glucagon precursor |
| 20 | 78 | 50.3 | 72 | 1 | GCRT glucagon precursor |
| 21 | 77 | 49.7 | 29 | 1 | GCRT glucagon precursor |
| 22 | 77 | 49.7 | 144 | 1 | GCRT glucagon precursor |
| 23 | 76 | 49.0 | 30 | 2 | S44473 glucagon precursor |
| 24 | 76 | 49.0 | 153 | 1 | A28406 glucagon precursor |
| 25 | 75 | 48.4 | 42 | 1 | GIBO glucagon precursor |
| 26 | 75 | 48.4 | 42 | 1 | GIBO glucagon precursor |
| 27 | 74 | 47.7 | 29 | 2 | S07211 glucagon precursor |
| 28 | 74 | 47.7 | 144 | 2 | S71426 glucagon precursor |
| 29 | 72 | 46.5 | 29 | 1 | A61583 glucagon precursor |

| | | | | | |
|-----|------|------|------|---|---------------------------|
| 30 | 72 | 46.5 | 29 | 1 | GCDF glucagon precursor |
| 31 | 72 | 46.5 | 29 | 1 | GCDF glucagon precursor |
| 32 | 72 | 46.5 | 29 | 1 | GCDF glucagon precursor |
| 33 | 72 | 46.5 | 29 | 1 | GCDF glucagon precursor |
| 34 | 72 | 46.5 | 29 | 2 | A91740 glucagon precursor |
| 35 | 72 | 46.5 | 29 | 2 | C39258 glucagon precursor |
| 36 | 72 | 46.5 | 29 | 2 | A91742 glucagon precursor |
| 37 | 72 | 46.5 | 29 | 2 | A91741 glucagon precursor |
| 38 | 72 | 46.5 | 87 | 1 | GCRT glucagon precursor |
| 39 | 72 | 46.5 | 124 | 1 | GCRT glucagon precursor |
| 40 | 71 | 45.8 | 29 | 2 | S39018 glucagon precursor |
| 41 | 70 | 45.2 | 29 | 1 | GCRT glucagon precursor |
| 42 | 70 | 45.2 | 29 | 2 | A61135 glucagon precursor |
| 43 | 69 | 44.5 | 30 | 2 | C61125 glucagon precursor |
| 44 | 69 | 44.5 | 30 | 2 | B61125 glucagon precursor |
| 45 | 67 | 43.2 | 29 | 1 | GCRT glucagon precursor |
| 46 | 65 | 41.9 | 29 | 2 | GCRT glucagon precursor |
| 47 | 65 | 41.9 | 39 | 1 | HMGR32 glucagon precursor |
| 48 | 65 | 41.9 | 679 | 2 | C71413 glucagon precursor |
| 49 | 63 | 40.6 | 31 | 2 | S44472 glucagon precursor |
| 50 | 62.5 | 40.3 | 928 | 2 | C37271 glucagon precursor |
| 51 | 62 | 40.0 | 2172 | 2 | T20145 glucagon precursor |
| 52 | 61 | 39.4 | 31 | 2 | S44471 glucagon precursor |
| 53 | 61 | 39.4 | 502 | 2 | H75290 glucagon precursor |
| 54 | 61 | 39.4 | 1075 | 1 | OYRTHX glucagon precursor |
| 55 | 60 | 38.7 | 39 | 1 | HMGR4G glucagon precursor |
| 56 | 60 | 38.7 | 344 | 2 | S64931 glucagon precursor |
| 57 | 60 | 38.7 | 639 | 2 | A86845 glucagon precursor |
| 58 | 59 | 38.1 | 145 | 2 | A60038 glucagon precursor |
| 59 | 58 | 37.4 | 36 | 2 | D60840 glucagon precursor |
| 60 | 58 | 37.4 | 460 | 2 | T39462 glucagon precursor |
| 61 | 57.5 | 37.1 | 170 | 1 | VRRRT glucagon precursor |
| 62 | 57 | 36.8 | 170 | 1 | A60037 glucagon precursor |
| 63 | 57 | 36.8 | 170 | 1 | S56795 glucagon precursor |
| 64 | 57 | 36.8 | 347 | 2 | T14096 glucagon precursor |
| 65 | 56.5 | 36.5 | 1849 | 2 | B69881 glucagon precursor |
| 66 | 56.5 | 36.5 | 388 | 2 | C89914 glucagon precursor |
| 67 | 56 | 36.1 | 233 | 2 | AH3154 glucagon precursor |
| 68 | 56 | 36.1 | 311 | 2 | AH3154 glucagon precursor |
| 69 | 56 | 36.1 | 326 | 2 | A99133 glucagon precursor |
| 70 | 56 | 36.1 | 896 | 2 | S61996 glucagon precursor |
| 71 | 56 | 36.1 | 1073 | 1 | OYRTHX glucagon precursor |
| 72 | 55.5 | 35.8 | 255 | 2 | T38115 glucagon precursor |
| 73 | 55.5 | 35.8 | 365 | 2 | B83952 glucagon precursor |
| 74 | 55.5 | 35.8 | 443 | 2 | T35974 glucagon precursor |
| 75 | 55.5 | 35.8 | 688 | 2 | AH2294 glucagon precursor |
| 76 | 55.5 | 35.8 | 881 | 2 | AE2153 glucagon precursor |
| 77 | 55 | 35.5 | 388 | 2 | H64427 glucagon precursor |
| 78 | 55 | 35.5 | 2054 | 2 | T32413 glucagon precursor |
| 79 | 54 | 34.8 | 920 | 2 | T40863 glucagon precursor |
| 80 | 54 | 34.8 | 920 | 2 | T40771 glucagon precursor |
| 81 | 54 | 34.8 | 968 | 2 | C84452 glucagon precursor |
| 82 | 54 | 34.8 | 1088 | 2 | C84054 glucagon precursor |
| 83 | 53.5 | 34.5 | 254 | 1 | BVBY53 glucagon precursor |
| 84 | 53.5 | 34.5 | 606 | 2 | S57552 glucagon precursor |
| 85 | 53.5 | 34.5 | 720 | 2 | T25883 glucagon precursor |
| 86 | 53.5 | 34.5 | 1174 | 2 | AE2911 glucagon precursor |
| 87 | 53.5 | 34.5 | 1174 | 2 | C97686 glucagon precursor |
| 88 | 53 | 34.2 | 320 | 2 | A24815 glucagon precursor |
| 89 | 53 | 34.2 | 325 | 2 | B90764 glucagon precursor |
| 90 | 53 | 34.2 | 330 | 2 | T26317 glucagon precursor |
| 91 | 53 | 34.2 | 349 | 2 | D85678 glucagon precursor |
| 92 | 53 | 34.2 | 349 | 2 | H85626 glucagon precursor |
| 93 | 53 | 34.2 | 349 | 2 | B90819 glucagon precursor |
| 94 | 53 | 34.2 | 380 | 2 | E80912 glucagon precursor |
| 95 | 53 | 34.2 | 380 | 2 | E81302 glucagon precursor |
| 96 | 53 | 34.2 | 414 | 2 | A81655 glucagon precursor |
| 97 | 53 | 34.2 | 490 | 2 | T32057 glucagon precursor |
| 98 | 53 | 34.2 | 571 | 2 | T67337 glucagon precursor |
| 99 | 53 | 34.2 | 714 | 1 | CIHMH glucagon precursor |
| 100 | 52.5 | 33.9 | 79 | 2 | AB1982 glucagon precursor |
| 101 | 52.5 | 33.9 | 863 | 2 | B71343 glucagon precursor |
| 102 | 52 | 33.5 | 55 | 1 | VRRB glucagon precursor |

glucagon - smaller
glucagon - duck
glucagon - North A
glucagon - slider
glucagon - turkey
glucagon - common
glucagon - Arabian
glucagon - rabbit
glucagon precursor
glucagon I precursor
glucagon - bowfin
glucagon - Europea
glucagon - bigeye
glucagon-like peptide
glucagon-like peptide
glucagon - Chinchi
glucagon I - Euro
glucagon - Mexico
glucagon G2 - Nort
A-alpha Y 4 protei
hypothetical prote
glucagon G1 - Nort
hypothetical prote
heat-stable entero
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